FIG.1

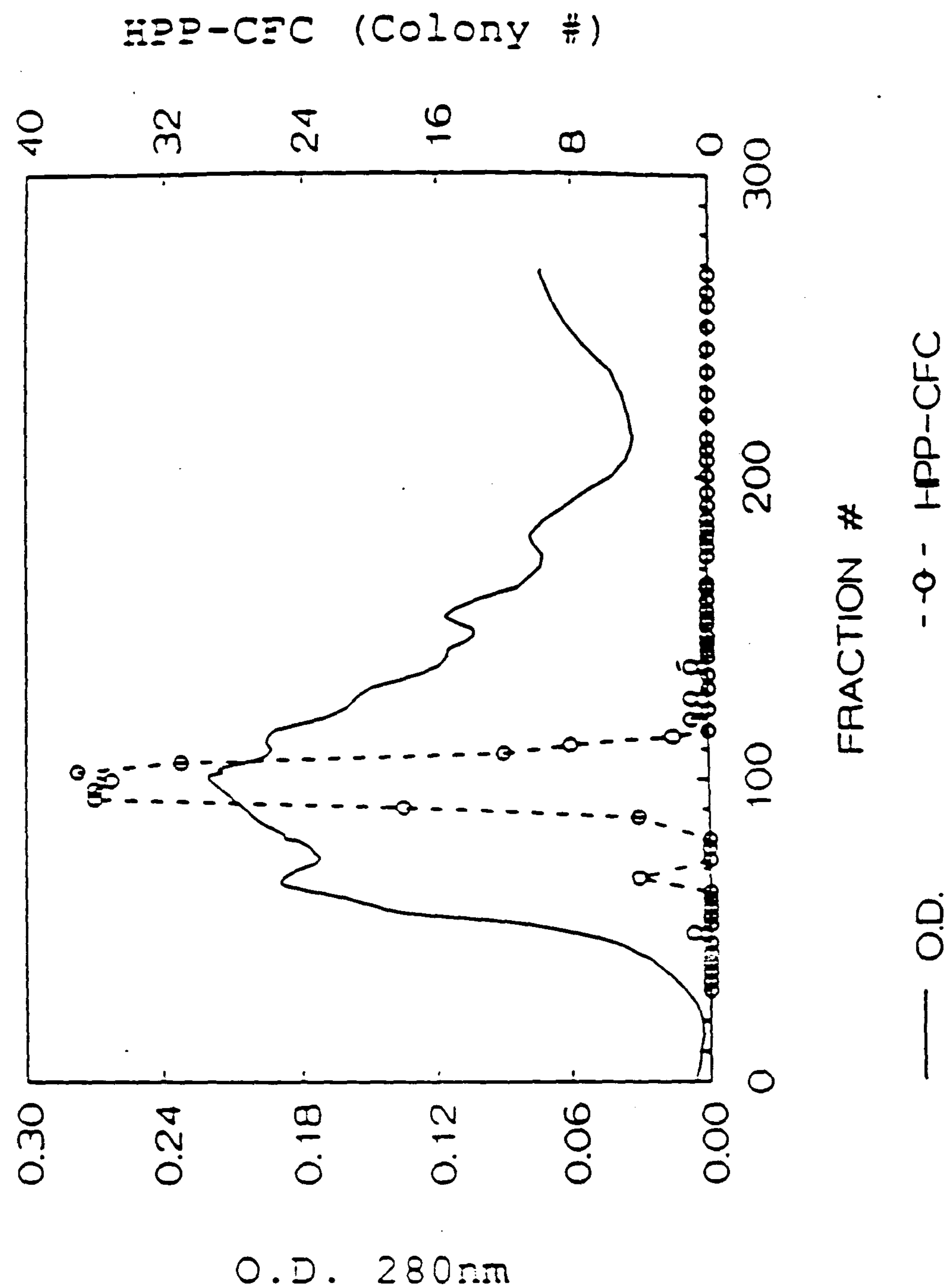
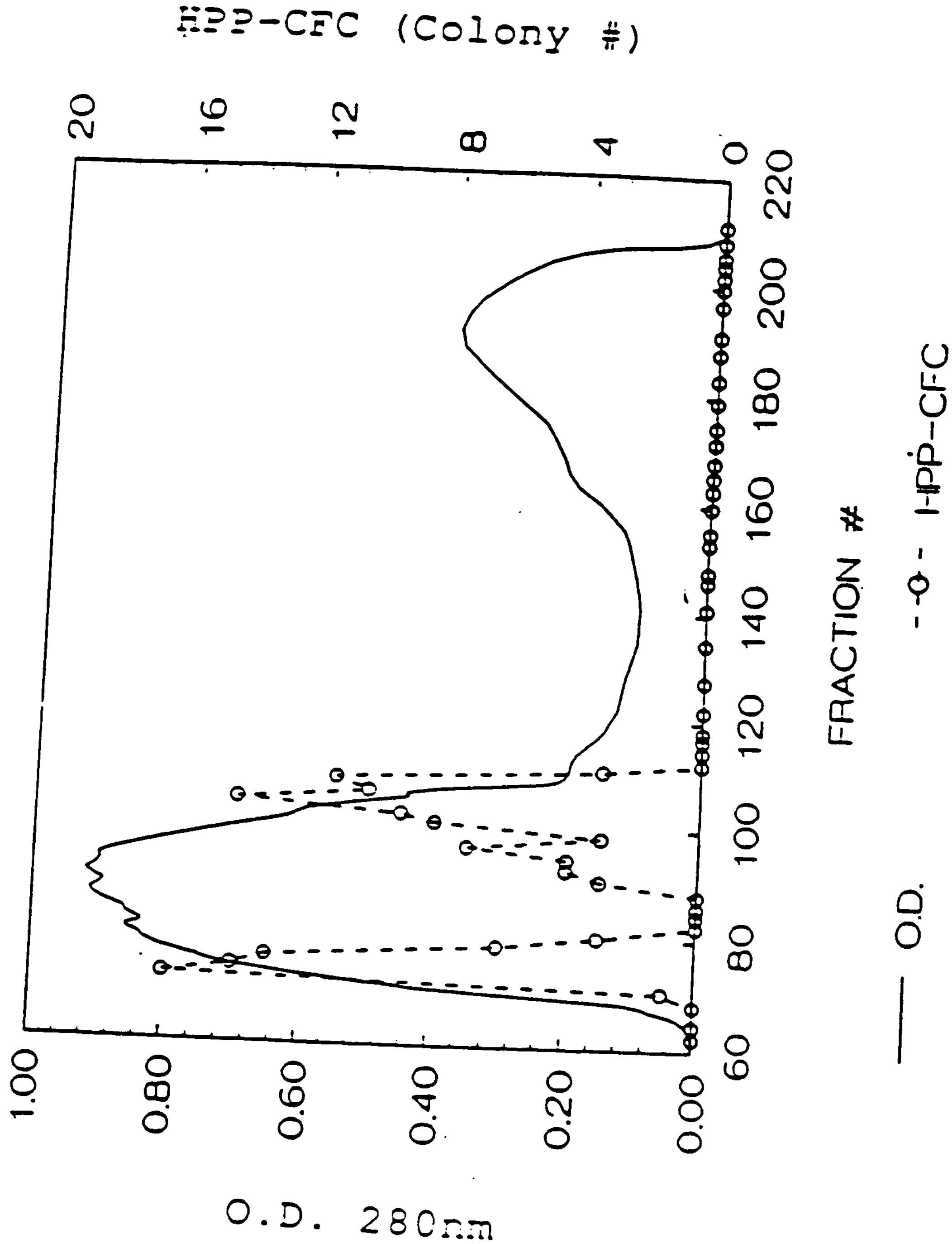

HPP-CFC (Colony #)
40
32
24
16
8
0
0.30
0.24
0.18
0.12
0.06
0.00
0
100
200
300
FRACTION #
O.D.
HPP-CFC
O.D. 280nm

FIG.2



HPP-CFC (Colony #)
20
16
12
8
4
0
1.00
0.80
0.60
0.40
0.20
0.00
60
80
100
120
140
160
180
200
220
FRACTION #
O.D.
HPP-CFC
O.D. 280nm

FIG.3

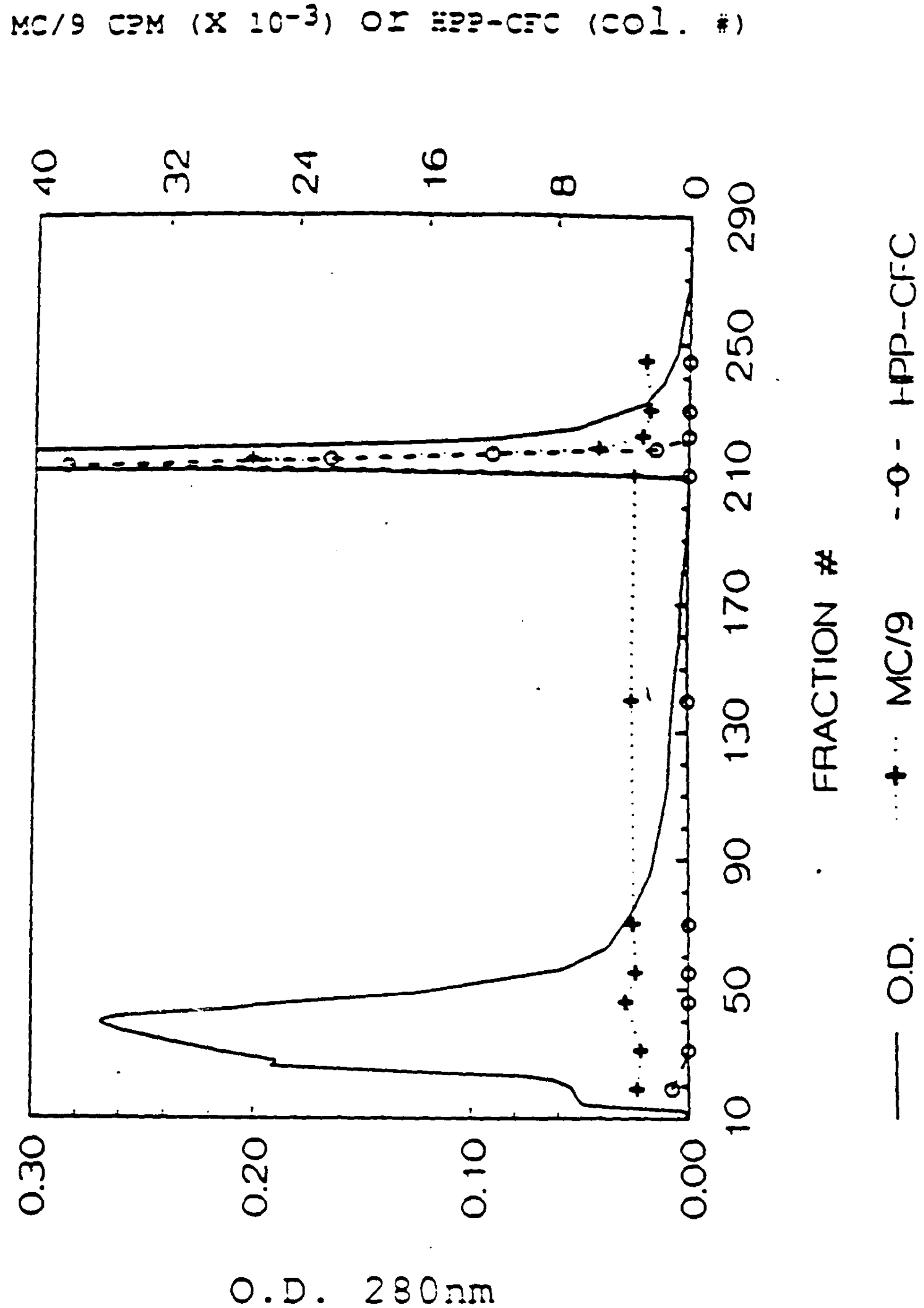
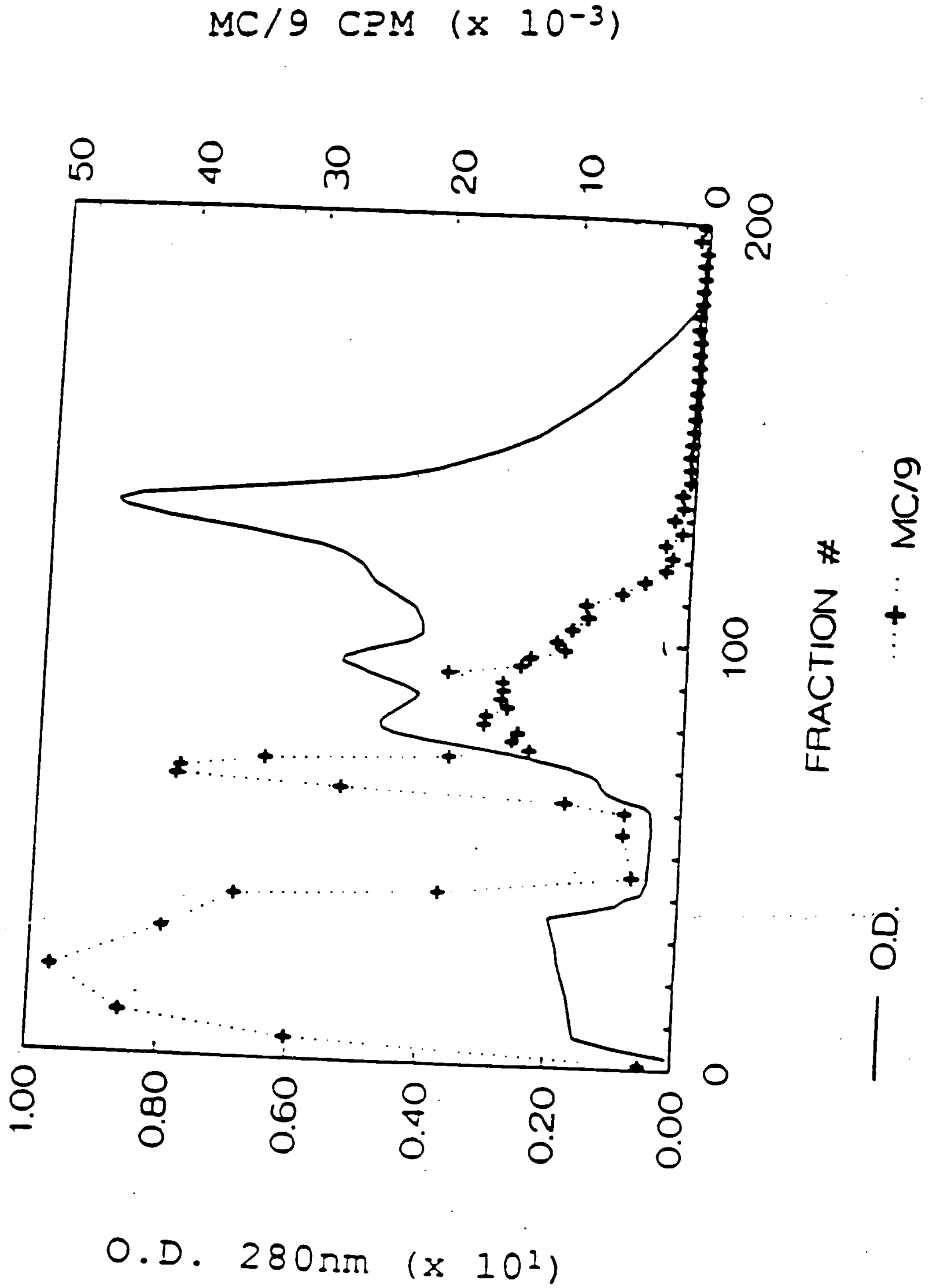

MC/9 CPM (X 10^{-3}) or HPP-CFC (col. #)
40
32
24
16
8
0
0.30
0.20
0.10
0.00
10
50
90
130
170
210
250
290
FRACTION #
— O.D.
+ MC/9
-o- HPP-CFC
O.D. 280nm

FIG. 4



MC/9 CPM (x 10^-3)
50
40
30
20
10
0
0
100
200
FRACTION #
O.D.
MC/9
1.00
0.80
0.60
0.40
0.20
0.00
O.D. 280nm (x 10^1)

FIG.5

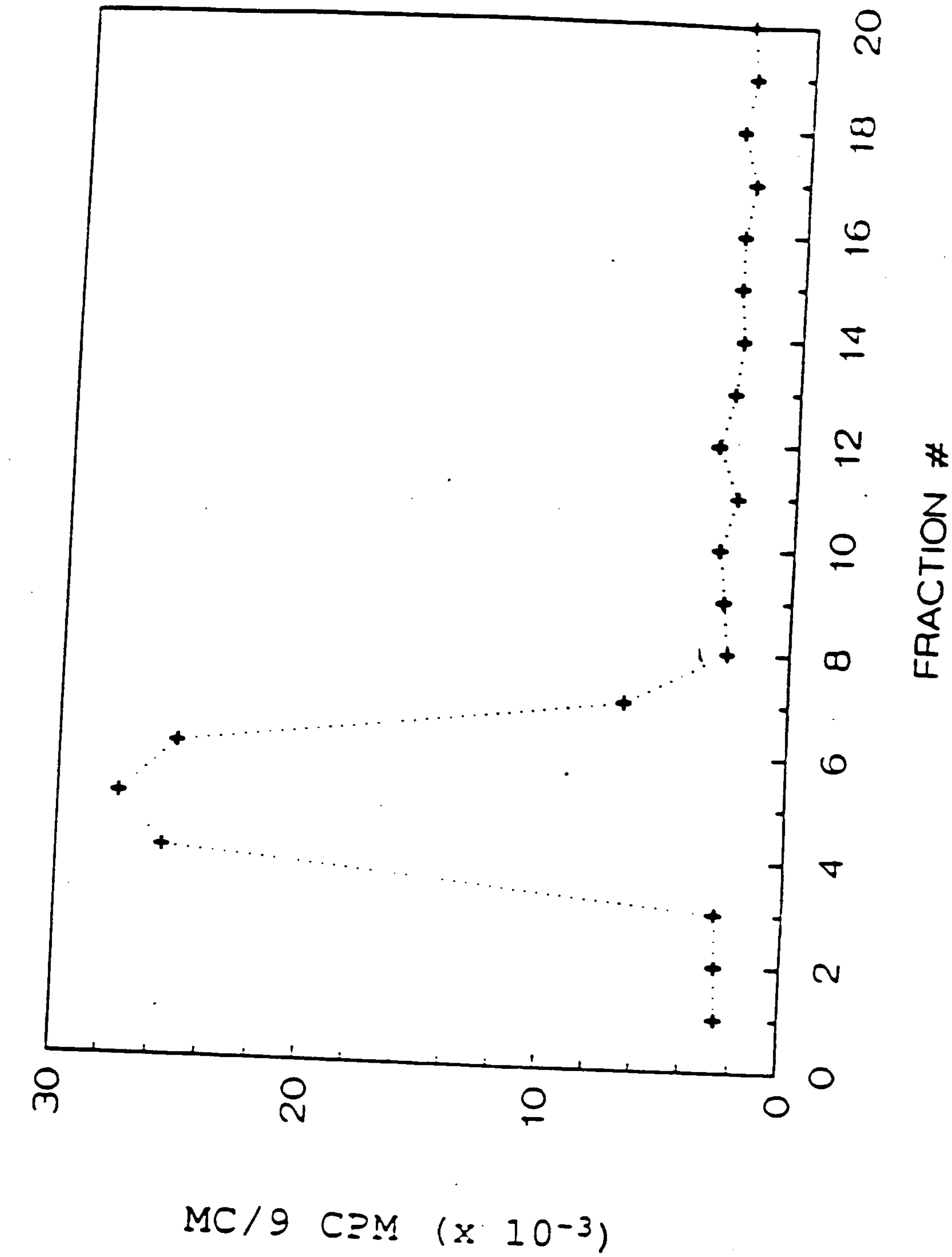


FIG. 6

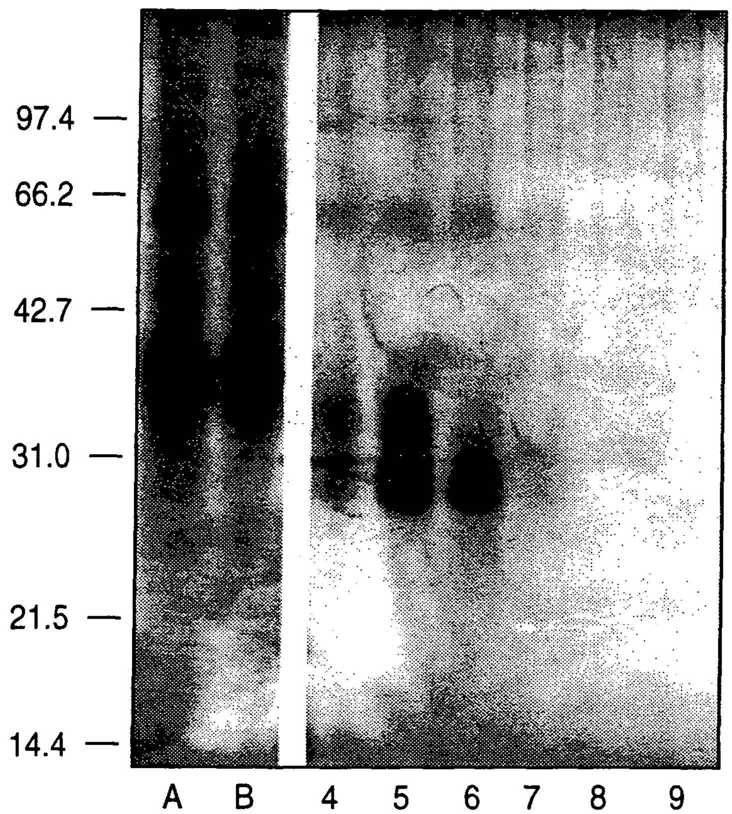


FIG. 7

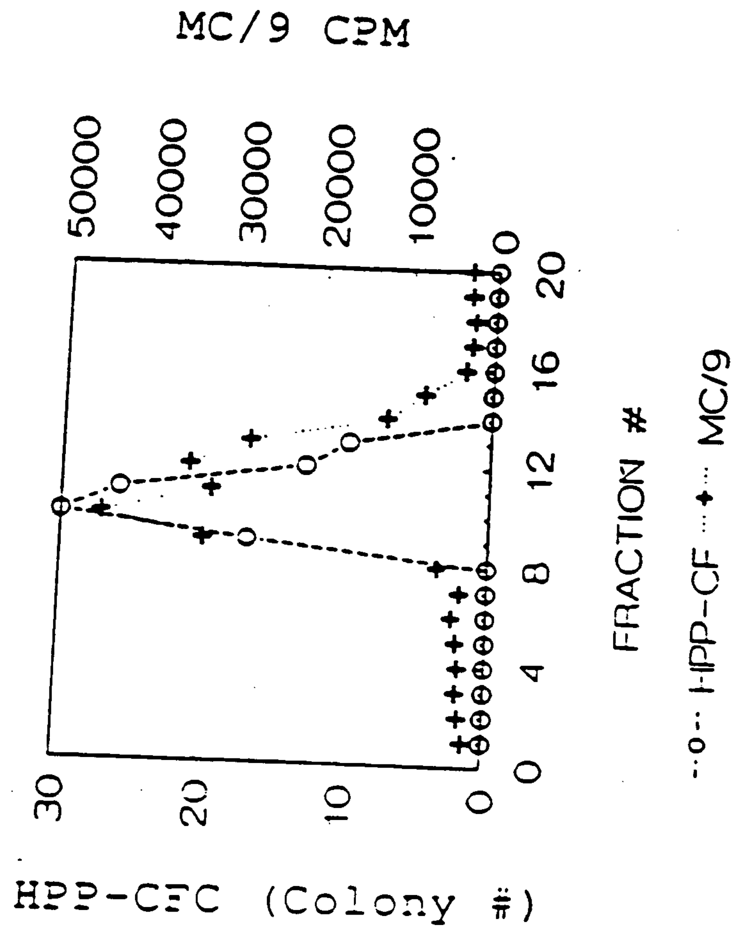

MC/9 CPM
50000
40000
30000
20000
10000
0
30
20
10
0
0
4
8
12
16
20
FRACTION #
HPP-CF
MC/9
HPP-CFC (Colony #)

FIG. 8

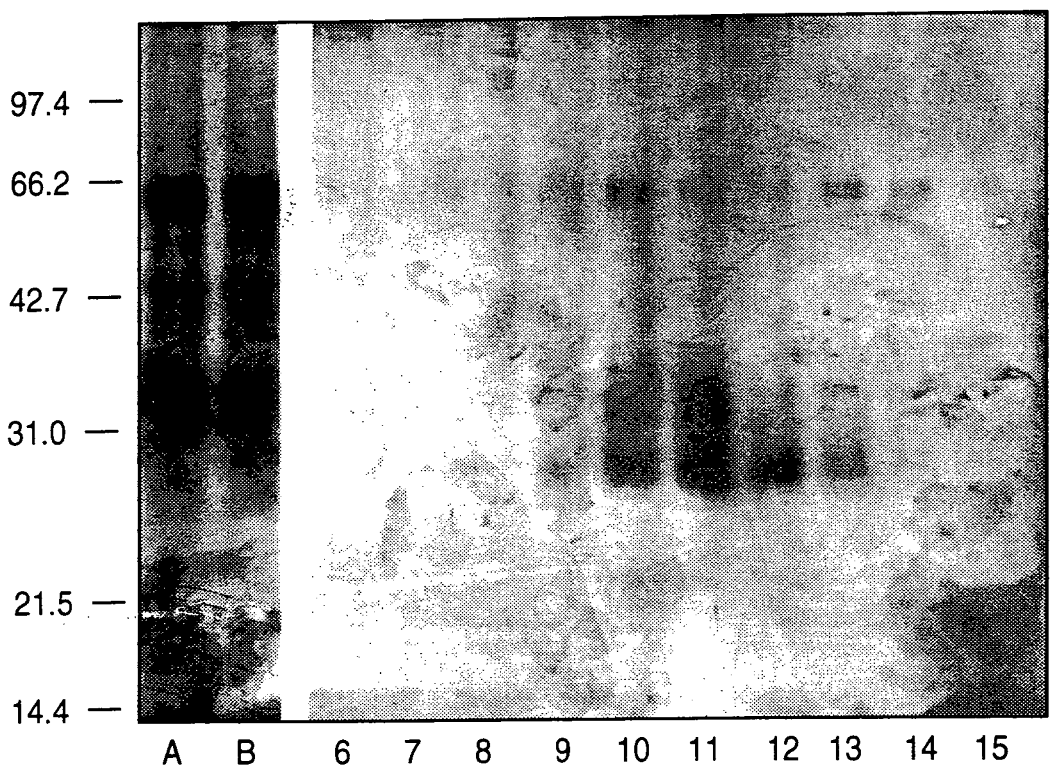
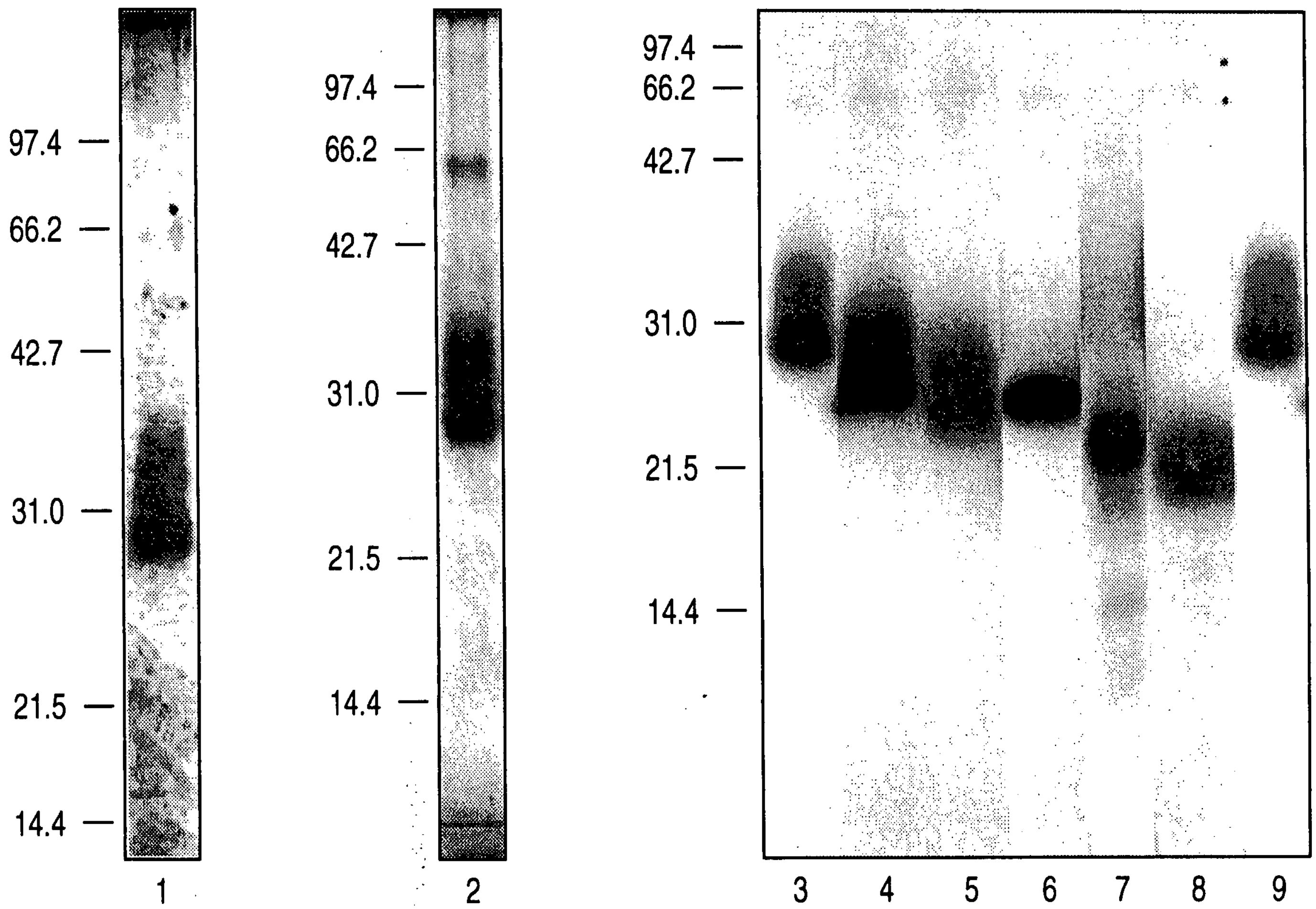


FIG. 9



97.4
66.2
42.7
31.0
21.5
14.4
1
97.4
66.2
42.7
31.0
21.5
14.4
2
97.4
66.2
42.7
31.0
21.5
14.4
3
4
5
6
7
8
9

FIG.10

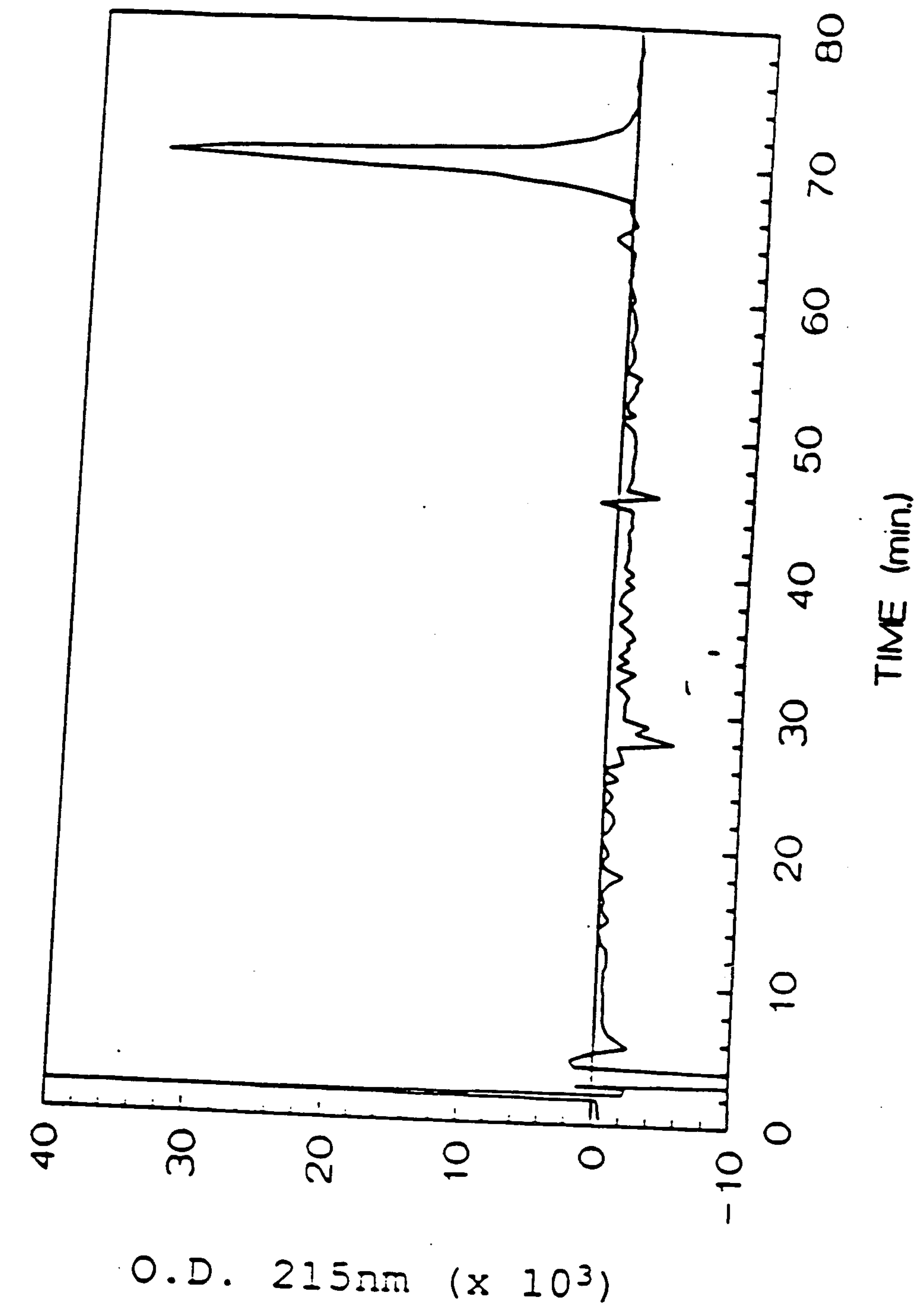


FIG.11

```
1                                       10                                      20
pE E I C R N P V T D N V K D I T K L V A N L P N D
 |------------------------------------------------ Sequencing after
                                                   |-------- T-5a -------

          30                                      40                          50
Y M I T L N Y V A G M D V L P S H C W L R D M V T
<Glu Aminopeptidase Treatment -------------->
                                                         |-----------------
------------------------------------------ T-5a ---------------|
   |--------- CB-6a ---------||-------- CB-8; CB-10 ---------|
                                    60                                 70
H L S V S L T T L L D K F S N I S E G L S N Y S I
------ Sequencing after Trp Cleavage ----------------

         80                                        90                        100
I D K L G K I V D D L V A C M E E N A P K N V K E
--------------------------->
                      :------------------- T-3 --------------------|        ---
                                                                            |--
                                                   |-CB-14;CB-15;CB-16 -
                                                       |-------- S-1---------|
                                    110                               120
S L K K P E T R N F T P E E F F S I F N R S I D A
--- T-1 ----------------:---- T-4(N109 nonglyco) -----||-----------
----- T-7(N120 glyco);T-8(N109 nonglyco)-----:
--------------------------- CB-14; CB-15; CB-16 -------------------
|----------------- S-5 or S-6 (N109 nonglyco)-----------------
     130                                        140                          150
F K D F M V A S D T S D C V L S S T L G P E K D S
----------------------------- T-5b --------------------------------------
-----------------:--------------------------- CB-6B ---------------------------
------ S-5 or S-6----------.                                                   -
                                    160
R V S V T K P F M L P P V A(A)
--||----- T-2 ---:                      <-- <-- (Carboxypeptidase)
------ CB-6B ----------
------------------- S-2 ----------------------|
```

FIG.12A

OLIGO	SEQUENCE	LOCATION
219-21	ACATTCTTIGGIGCATTCTCCTCCAT	393-368
	G T G T T	
219-22	AAAAACTCCTCIGGIGTAAAATT	447-425
	G T T G G	
219-25	GTTTCNGGTTTTTT	420-407
	C C C	
219-26	ATGGAAGAAAACGCCCCCAAAAACGT	368-393
	G G T G T	
222-11	CCNAATGATTATATGATAAC	167-186
	C C C C	
	T	
222-12	GGNGGNAACATAAANGGCTT	566-585
	G G T	
223-6	ACCATAAAATCTTTAAAICGATC	492-470
	G G C G G	
224-24	GTATTTTCAATAGATCCATTGA	450-471
224-25	CCAACTATGTCGCC	190-202
224-27	GTAGTCAAGCTGACTGATAAG	273-253

FIG.12A CONT.'

224-28	TAACCAACAATGACTAGGCAA	235-215	
225-31	TTCCAGAGTCAGTGTC	547-562	
227-29	GCGAAGCTTGCCTTTCCTTATGAAGAAGA	16-35	*
227-30	GCGCCGCGGTTACGGTGGTAACATGAAGGGCTTTGTGA	586-561	*
228-30	GATAAATGCAAGTGATAATCC	45-65	
230-25	GCGGTCGACCCGCGGAACTTTAAGTCCATGCAACAC	705-685	*
237-19	CACCCGCGGTTATGCAACAGGGGGTAACATAAATGG	569-592	*
237-20	CACCCGCGGTTAGGCTGCAACAGGGGGTAACATAAA	572-595	*

FIG.12B

OLIGO	SEQUENCE	LOCATION
231-27	CTTAATGTTGAAGAAACC	703-686
233-13	GATGGTAGTACAATTGTCAGAC	410-431
233-14	GTCTGACAATTGTACTACCATC	431-410
235-29	CAATTTAGTGACGTCTTTTACA	302-323
235-30	TTAGATGAGTTTTCTTTCACGCAC	556-533
235-31	AAATCATTCAAGAGCCCAGAACCC	566-589
236-31	AACATCCATCCCGGGGAC	366-383
238-31	CTGGCAATATTTTAAGTCTCAAGAAGACC	
241-6	GCGCCGCGGCTCCTATAGGTGCTAATTGG	
254-9	CCTCACCACTGTTTGTGCTGGATCGCA	153-179
262-13	GGTGTCTAGACTTGTGTCTTCTTCATAAGGA	209-190

FIG. 12C

OLIGO	SEQUENCE
201-7	CCCCCCCCGG T A
220-3	TTTTTTTTTTTTTTTTTTGG
220-7	TTTTTTTTTTTTTTTTTTAG
220-11	TTTTTTTTTTTTTTTTTTCG
221-11	TTCGGCCGATCAGGCCCCCCCCCC
221-12	TTCGGCCGGATAGGCCTTTTTTTTTTTTTTT
228-28	GGCCGGATAGGCCTCACNNNNNNT
228-29	GGCCGGATAGGCCTCAC

FIG.13A

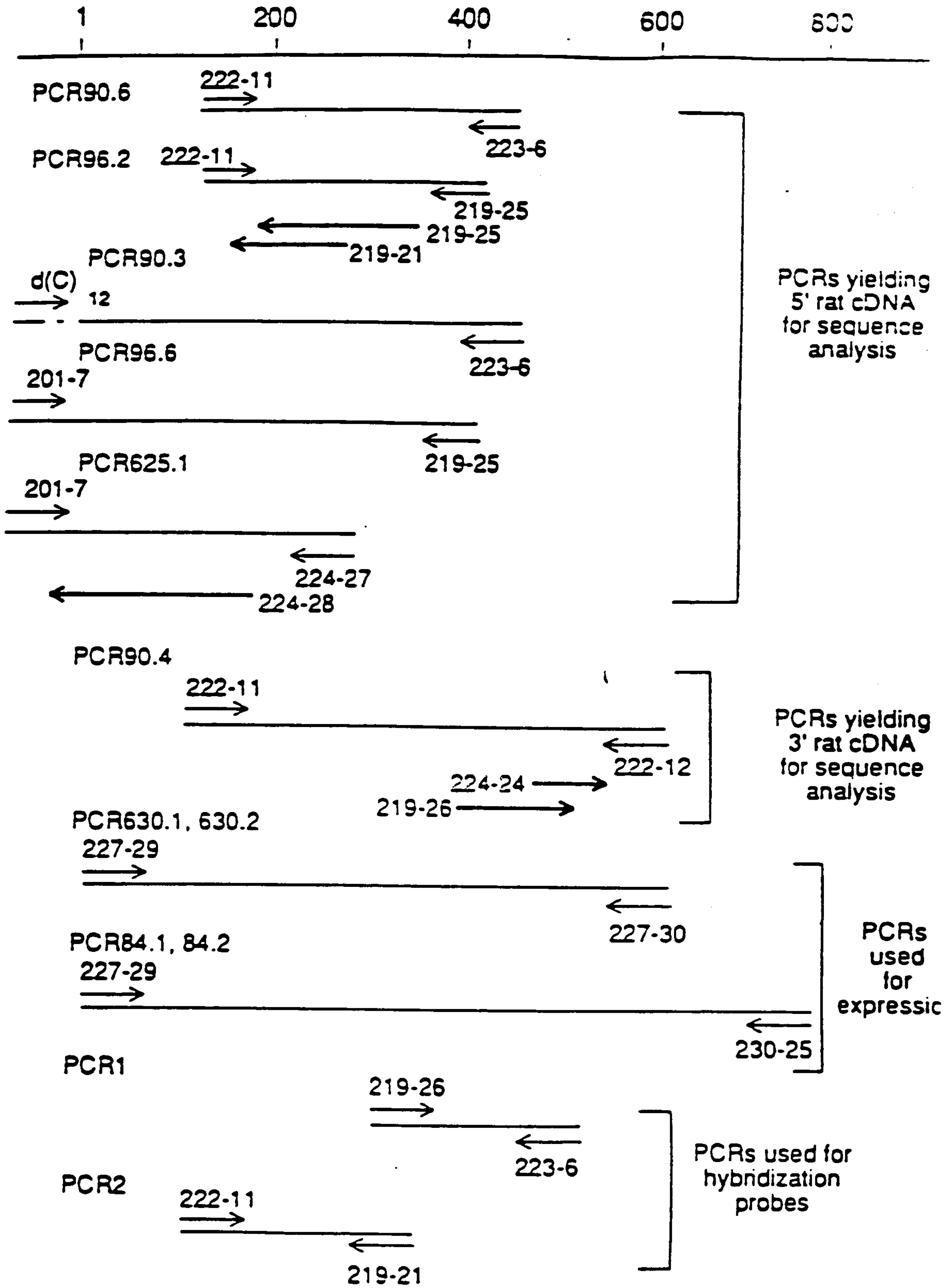

1
200
400
600
800
PCR90.6
222-11
223-6
PCR96.2
222-11
219-25
219-25
219-21
PCR90.3
d(C)
12
223-6
PCR96.6
201-7
219-25
PCR625.1
201-7
224-27
224-28
PCRs yielding 5' rat cDNA for sequence analysis
PCR90.4
222-11
222-12
224-24
219-26
PCRs yielding 3' rat cDNA for sequence analysis
PCR630.1, 630.2
227-29
227-30
PCR84.1, 84.2
227-29
230-25
PCRs used for expressic
PCR1
219-26
223-6
PCR2
222-11
219-21
PCRs used for hybridization probes

FIG.13B

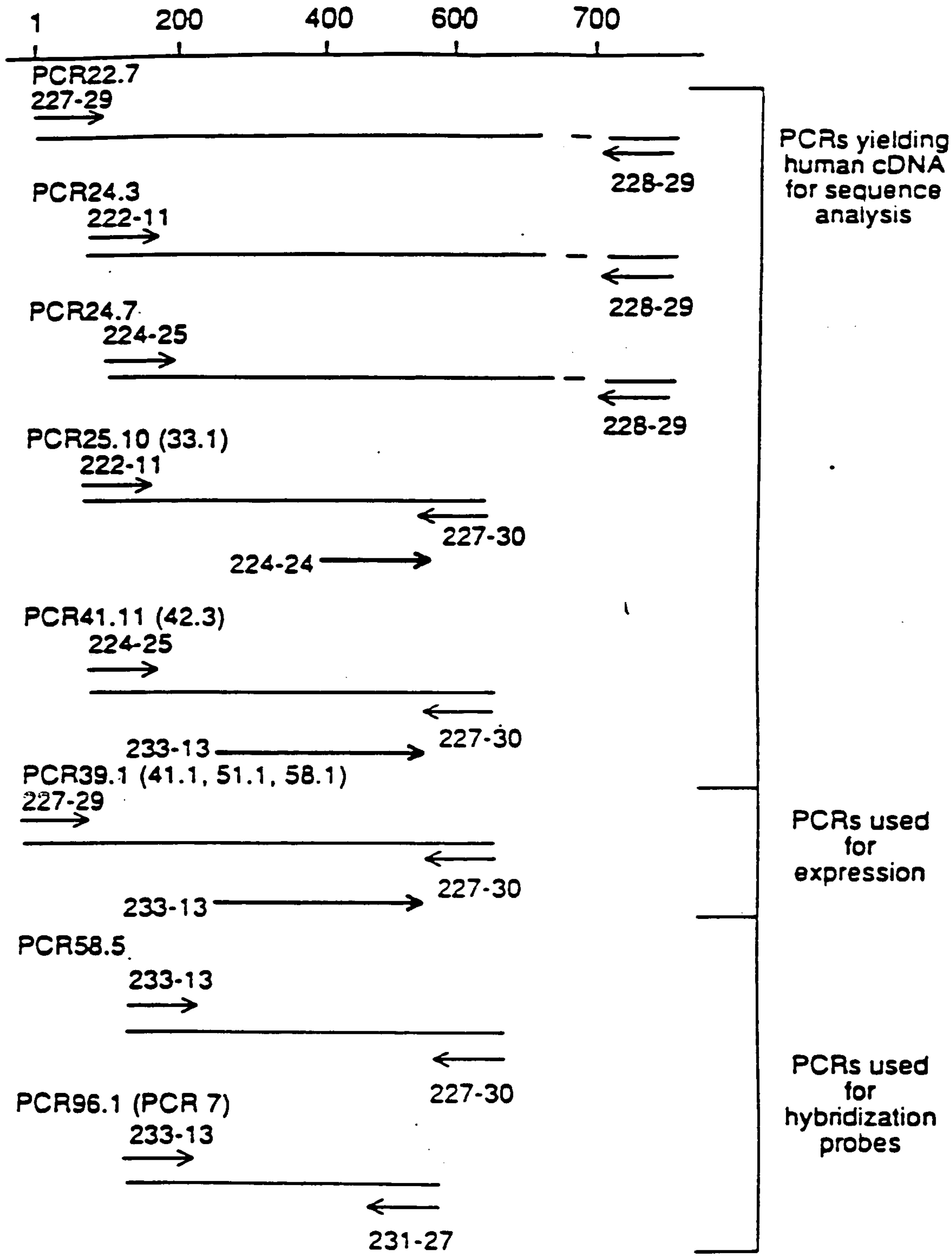

1
200
400
600
700
PCR22.7
227-29
228-29
PCR24.3
222-11
228-29
PCR24.7
224-25
228-29
PCR25.10 (33.1)
222-11
227-30
224-24
PCR41.11 (42.3)
224-25
227-30
233-13
PCR39.1 (41.1, 51.1, 58.1)
227-29
227-30
233-13
PCR58.5
233-13
227-30
PCR96.1 (PCR 7)
233-13
231-27
PCRs yielding human cDNA for sequence analysis
PCRs used for expression
PCRs used for hybridization probes

FIG.14A

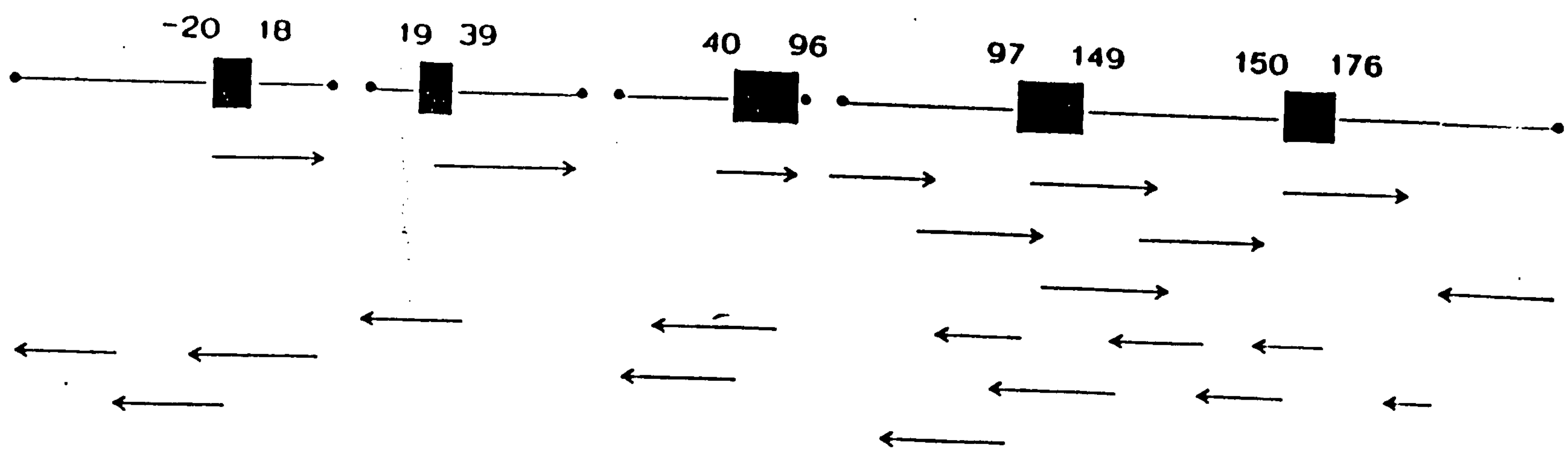


FIG.14B

```
AAAGTATCTTTCTATTGGCGAAGGACATGTTTTCCcATAAGTGGT     45

AAACAnACTGTCTGCACATAATAATTATCTTGCTGCCGTAAAGAT     90

TAGGTTAAATTCTGcCTTCGATCTAAAAACACACCCTTCTGTCAA    135

TCCGAGGAGCAGTGTGCTAGTCTAGAGGTCTAAATGAAGGCTCCT    180

TTCACGGTTGTATTTCTGCTCCCCAAATTGTCCACATTTAAAAGG    225

AGAGTGCTTCTTTTCAGCCTTAGGCTCTGAATTTCATGCATTCCT    270

CCATTTTCCGAGGTCCCccCcAAGTGATAATTCTGTTACACGTTG    315

CTACAAGTTCATCCCTAATTGCCGTCAAGAAACTGACTGTAGAAG    360

GCTTACCACAGACGTTGTAACCGACAGTAAAGCCATTGAAAGAGT    405

AATTCAAACAGGATGGAAGCCAGGAGTATTTTGTGGCTGTTGCTC    450

TTTTTCTTTTCAGTTTGGTGAGAGCAGCTTGAATGCTTAACATTT    495

AAGCCATCAGCTTAAAACAAAACAAAACAAAACAAAAAAAAACCC    540

CGCTCTGGCATATTTGCACTTAACACATACGGTATAAGGTGTTAC    585

TGGTTTGCATAGTTCTGGATTTTTTTTTTTTAAAAACTGATGGAC    630

                             -20
                             ThrTrpIleIleThrC
ACCAAGAAATGTTTCTGTTCTTTGTTTAGACTTGGATTATCACTT    675

          -10
ysIleTyrLeuGlnLeuLeuLeuPheAsnProLeuValLysThrG
GCATTTATCTTCAACTGCTCCTATTTAATCCTCTCGTCAAAACTC    720

 1                          10
lnGluIleCysArgAsnProValThrAspAsnValLysAspIleT
AGGAGATCTGCAGGAATCCTGTGACTGATAATGTAAAAGACATTA    765

    18
hrLysLeu
```

FIG.14B CONT.'

```
CAAAACTGGTAAGTAAAGAATGATTTTGGCATCTATAAGTCTTCC    810

CTGTGCTTGCTGACCACATAGGTTCAGGGCACTCCCGACAGGAGT    855

TCCCAGCTTTCTAAGATAAGGAATCACTGTACGAGTCTGAAGTGC    900

TTCTTCTGGGCAAATGGGAGATGCTTAGGTCATGGAGGGTTTATC    945

TGTATAACTGGCCCTTTGCACACCAACAAAGTGACTGACTGGCTT    990

TTGCCTGTTACCTACTG                               1007

    Intervening sequence of unknown length

TCTCCAGTCCTGGGCATGGTATATACTTAGGCACCCAAGATTGGA     45

TTTACAACTCAAGCATTATATATTGGACAACnACGGGGTATGAGA     90

TATTAATGATATGTCAGGTTGGATGGATGAGTTTTCTCAAGAAAT    135

                                           19
                                          Val
TCTCTTGTATTTACTCACGTTTTCATTTCTTGGTCTCTGTAGGTG    180

                            30
AlaAsnLeuProAsnAspTyrMetIleThrLeuAsnTyrValAla
GCGAATCTTCCAAATGACTATATGATAACCCTCAACTATGTCGCC    225

             39
GlyMetAspValLeu
GGGATGGATGTTTTGGTATGTAGTCCACACACTTCTGAGTTGCCT    270

TTTAGTAGCTAATGGGTGACCTGTGCTTATTCACATTGAAGACAT    315

TATTTGCTCTTTGTCGTTTTTAGATGTTGACCTATAATTTTTCCT    360

TCAAGCTGCTGCTAAGATTATCAGTGAGCATTTCAGTATGTGTTT    405

TAAGCCTACTCATTAAAAGGAAATGGCTCATCTTAGACGTAGCAA    450
```

FIG.14B CONT.'

CCGATGTTAATTTTTCCCCAGGCATCTCTCAGAGGGACTTGAATG 495

TTAAAATCATGTTAAATTTCCTCCTTGGCTATGTTATTTCTCATG 540

GCTATGTTATTCCTATTCGTATTTCATTTAAAGGGACGGAATATT 585

TATTGTATTTCTGAACTTTTTCAGGCATGCATCCGGGTCTTTGAA 630

TAAAA 635

Intervening sequence of unknown length

CACTAAGACTCCTTCTAGTAATGTTTGTAATCCTGTCTGTATCGA 45

ATGTCTTTGAAAACGCAGTGACTAAGCCATAAATAATCTTCCACA 90

GAACGTCCAGTGGTTCATGAACTTTGTATGTGGGGTGGGGCAAG 135

AATTGTCTCACTATTGGTCAAGGAAGAGAAGGTAAGGTATGCAAG 180

GGTGGTTTAATCTTCTTCCGTGGAAGGACAAAATCATCTATCATT 225

TCCTCTGATCTCTATGCATTTGTTTGTTTTGAACTGAATCTGACT 270

TGAGCAAGAGTTGGCGTCCTGTGTTCTGAGGAAACTCTTTGTCCT 315

GCAGTCAGTGACTAAAAGTGCTGAGAGATCTGAAGAGCACTCTGA 360

ATCTGCCATATTTTTAATAGATGCTTTGTCTTCTCTTTGAATTTC 405

40. 50
ProSerHisCysTrpLeuArgAspMetValThrHisLeu
TTCCAGCCTAGTCATTGTTGGTTACGAGATATGGTAACACACTTA 450

60
SerValSerLeuThrThrLeuLeuAspLysPheSerAsnIleSer
TCAGTCAGCTTGACTACTCTTCTGGACAAGTTTTCAAATATTTCT 495

70 80
GluGlyLeuSerAsnTyrSerIleIleAspLysLeuGlyLysIle

FIG. 14B CONT.'

GAAGGCTTGAGTAATTATTCCATCATAGACAAACTTGGGAAAATA 540

90 96
ValAspAspLeuValAlaCysMetGluGluAsnAlaProLys
GTGGATGACCTCGTGGCATGTATGGAAGAAAATGCACCTAAGGTA 585

ACTTGGTATTCATCAGAATTATTTTTCTTATACT 619

Intervening sequence of unknown length

GAGCTCATGATGAGCAATTCACAACCACTTGTAATTCCAGCTCCA 45

GAGGACATTATCCCCTCTTTGGATGCCATAGGAATCTGCTCTCAA 90

ATATGTAGATACCACCTCTGCCACCTCAGCACATACATACACATA 135

ATTAAAAAATAGAAACATTAAAGGAGTTCCAATCAATCCTTATTC 180

TTTTCTGTATTCAGTATGCCCAGATGTAAATTCTAGGAATATGTT 225

TTAAAGGCTAATTCTTATTTTGTAATAAGCAGCTTTAAAATTCTT 270

AATTGTTTTTTCGGGTCACTTTATTGTCCTATTGCCACGACATTG 315

TCCTGTCCCATTGTCTGTTATTCCTTCTGTTTTGTTTATTGTTCC 360

CTAGTTACTTTGATCATGAGATTGACCTGTTACCCGTTGTTATTC 405

TCTGTAGCCATTTTGAGTTGTGTCTATTAGAACAGCTGTTAAATT 450

ACTTGAATCATTGAGGACATAGTCAATAATCTATTATGCTGATCC 495

AGTCAAGTCTATGAGTTATTTGAAAACTAGAATCTTTGTTAATTA 540

97
AsnValLys
TTTGTTTGCTTGTTTGTTTGTTTATTATTTGTCTAGAATGTAAAA 585

100 110
GluSerLeuLysLysProGluThrArgAsnPheThrProGluGlu

FIG.14B CONT.'

GAATCACTGAAGAAGCCAGAAACTAGAAACTTTACTCCTGAAGAA 630

120
PhePheSerIlePheAsnArgSerIleAspAlaPheLysAspPhe
TTCTTTAGTATTTTCAATAGATCCATTGATGCCTTCAAGGACTTC 675

130 140
MetValAlaSerAspThrSerAspCysValLeuSerSerThrLeu
ATGGTGGCATCTGACACTAGTGATTGTGTGCTCTCTTCAACATTA 720

148
GlyProGluLysA
GGTCCTGAGAAAGGTAAGGCTTTTAAGCATTTCTTGTTTAAATGT 765

ACATAGAAAGCCTGAACTTCTGTAAGCCTCTACTGCTGAATCAAC 810

TAAATGTGTTGCTGTAGAAAGAACGTGTGGGTTTTTCTGATAAAA 855

ACAAAAAGCAAATATCAATGACTACCAATGATTATTATCTAGCTT 900

GAGAGATATGCCCTAAGACAGCGATTCTCGATATTTCTAAATTAA 945

AGAATTGTGTGATGGTGGCTCACATATTTTCTAACTGTGATATTT 990

GCCAGGAGAGTAGAATAATGTTATTCTTCATCCCCAGAATTCCTA 1035

AGATTTCACGTCTCATGTCTTTTCCATAAGGTTCAAACTCTGAGA 1080

CTTGAGTTCTGAGCCTCAGCAGGTCATTCTGAATCCCCACTCTCC 1125

CCGAGCTGGGTCCCTATGGGGAACTAACTTCATTGCTTTCTTTT 1170

AAAACATGACGAGTTACCAACAGCTCCTCGCTATTATAAACATGT 1215

TCCTAAGCATGTCTGTGCATGCaATAAGCCTTCACTCTACAAGAC 1260

AGTTATGGTGTATCGCTTGACAAAACTGAGCAGCCAAGCTGAGTA 1305

TGAAATAATAATCTAGACTTGGGAGGCAGACCCAGCACCTACTGT 1350

GATATTGCACTTCGCCTTTGGGGGACTCTATGATTCAAAAGTTCA 1395

FIG.14B CONT.

```
                                             150
                                          spSerArgV
CCATGTAACACTGACACATTATTGCTTTCTATTTAGATTCCAGAG   1440

                          160
alSerValThrLysProPheMetLeuProProValAlaAlaSerS
TCAGTGTCACAAAACCATTTATGTTACCCCCTGTtGCAGCCAGTT   1485

      170                    176
erLeuArgAsnAspSerSerSerSerAsn_
CCCTTAGGAATGACAGCAGTAGCAGTAATAGTAAGTACACATATC   1530

TGATTTACTGCATGCATGGCTCCAAGTATCCTCTATAGGAGTGTT   1575

GCATGGACTTAAAGTTTATAAATCACTACTAATAATGCTGTTCTG   1620

TCACTGTTATTCCTTGTATGGGCTTCCTGACAATTAAATATCTGG   1665

TTTGTAGAATCGGATCTCCTTAGAGGTTAAGATGACCATGACAAA   1710

ATTAGGCCAATCAACTTTCTGCGAAGGTTATTTTAAATAAGGCAC   1755

GAAATTAATTGAAGGAAAAAAAAAATACAAGCAAGGCCTTATTTTG   1800

AATCATGGTAGGCTTAAAATAGACTTTGTGGAGAATGTCCCTGAT   1845

CAAAGTGGAGTTTTCAGATTTCAAGTGCATGTGCTAACTCTCCAC   1890

AATGTCAAGGCTATTTTCAGTTTTGTGTCTCCATATTTACTACTG   1935

CATGTTTGGAAATTTGCTGATGCTGTTAGATTACCTAAGAATGTA   1980

TGTTGAAGAAGAATGGACTTCTTTCCCTAAAATTTCTGTCCTCTT   2025

TGcCCAAGAACCCAcGTTCCTGGAAGACTATCTTATTTTCATGTC   2070

TGTGCAATGATCATTATAAAGATTATTGAATATACTGGGAATACT   2115

CTGGTTTCTGTTTTTACAGATTCATAATAGCTTATTCAGTCTTTA   2160

AAGAAAGTTCTCTGAAGTCCATGCTTTAGAATGTTTCTCTATCAA   2205
```

FIG.14B CONT.'

AACTTGACCTGGACCTTAAATAAAGCTATATTTAGTCTTTTTATC 2250

CCTGAAAAATATATTTCACAGTGTAGACATTTGATATACATCTAA 2295

GGGAAGGATGCTGCCAGAATGCTCGGGCTGGCAGTCTACAAAGTC 2340

CACTGCTCTCAGGATGGACTTCTGAAAGCGGAAATTGTGAACTGC 2385

ATGCATATAACATATCAGATCCTCGAGC 2413

FIG.14C

```
                         -25            -20
                          M  K  K  T  Q  T  W  I  I  T  C  I
CTGGATCGCAGCGCTGCCTTTCCTTATGAAGAAGACACAAACTTGGATTATCACTTGCAT   60

     -10                                1
 Y  L  Q  L  L  L  F  N  P  L  V  K  T  Q  E  I  C  R  N  P
TTATCTTCAACTGCTCCTATTTAATCCTCTCGTCAAAACTCAGGAGATCTGCAGGAATCC  120

  10                             20
 V  T  D  N  V  K  D  I  T  K  L  V  A  N  L  P  N  D  Y  M
TGTGACTGATAATGTAAAAGACATTACAAAACTGGTGGCGAATCTTCCAAATGACTATAT  180

  30                             40
 I  T  L  N  Y  V  A  G  M  D  V  L  P  S  H  C  W  L  R  D
GATAACCCTCAACTATGTCGCCGGGATGGATGTTTTGCCTAGTCATTGTTGGTTACGAGA  240

  50                             60
 M  V  T  H  L  S  V  S  L  T  T  L  L  D  K  F  S  N  I  S
TATGGTAACACACTTATCAGTCAGCTTGACTACTCTTCTGGACAAGTTTTCAAATATTTC  300

  70                             80
 E  G  L  S  N  Y  S  I  I  D  K  L  G  K  I  V  D  D  L  V
TGAAGGCTTGAGTAATTATTCCATCATAGACAAACTTGGGAAAATAGTGGATGACCTCGT  360

  90                            100
 A  C  M  E  E  N  A  P  K  N  V  K  E  S  L  K  K  P  E  T
GGCATGTATGGAAGAAAATGCACCTAAGAATGTAAAAGAATCACTGAAGAAGCCAGAAAC  420

 110                            120
 R  N  F  T  P  E  E  F  F  S  I  F  N  R  S  I  D  A  F  K
TAGAAACTTTACTCCTGAAGAATTCTTTAGTATTTTCAATAGATCCATTGATGCCTTCAA  480
```

FIG.14C CONT.'

```
     130                                     140
  D    F    M    V    A    S    D    T    S    D    C    V    L    S    S    T    L    G    P    E
GGACTTCATGGTGGCATCTGACACTAGTGATTGTGTGCTCTCTTCAACATTAGGTCCTGA    540

     150                                     160
  K    D    S    R    V    S    V    T    K    P    F    M    L    P    P    V    A    A    S    S
GAAAGATTCCAGAGTCAGTGTCACAAAACCATTTATGTTACCCCCTGTTGCAGCCAGTTC    600

     170                                     180
  L    R    N    D    S    S    S    S    N    R    K    A    A    K    S    P    E    D    P    G
CCTTAGGAATGACAGCAGTAGCAGTAATAGGAAAGCCGCAAAGTCCCCTGAAGACCCAGG    660

     190                                     200
  L    Q    W    T    A    M    A    L    P    A    L    I    S    L    V    I    G    F    A    F
CCTACAATGGACAGCAATGGCACTGCCGGCTCTCATTTCGCTTGTAATTGGCTTTGCTTT    720

     210                                     220
  G    A    L    Y    W    K    K    K    Q    S    S    L    T    R    A    V    E    N    I    Q
TGGAGCCTTATACTGGAAGAAGAAACAGTCAAGTCTTACAAGGGCAGTTGAAAATATACA    780

     230                                     240
  I    N    E    E    D    N    E    I    S    M    L    Q    Q    K    E    R    E    F    Q    E
GATTAATGAAGAGGATAATGAGATAAGTATGTTGCAACAGAAAGAGAGAGAGTTTCAAGA    840

248
  V
GGTGTAATT                                                       849
```

FIG.15A

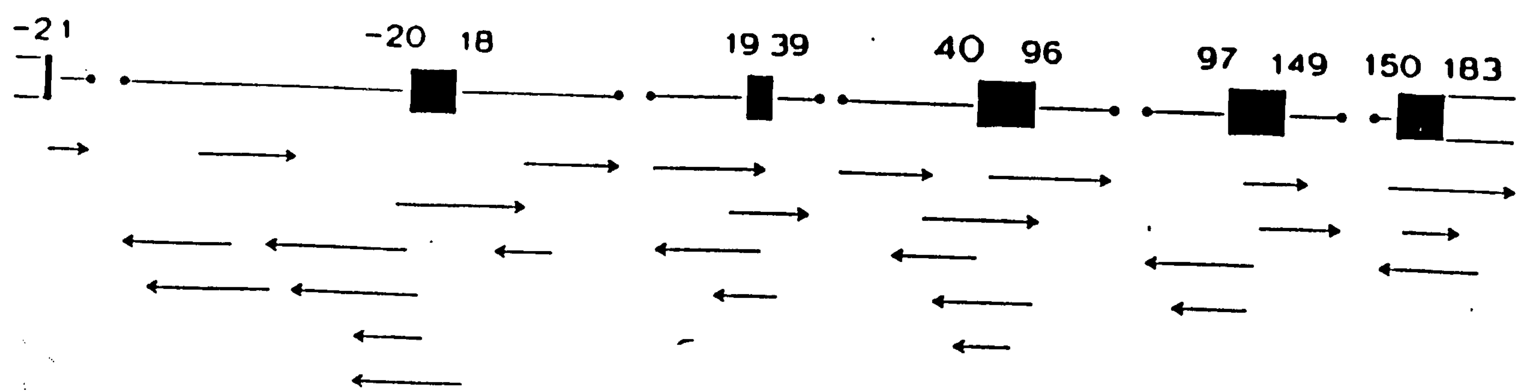


FIG.15B

-21
hrGln

CACAAGTGAGTAGGGCGCGCCCGGGAGCTCCCAGGCTCTCCAGGA 45

AAAATCGCGCCCGGTGCCCCGGGGaAGCCGGCGCTCCCTGGGACT 90

TGCAGCTGGGGCGTGCAGGGCTGTGCCTGCCGGGTG 126

Intervening sequence of unknown length

AGATACTACAAAGATAAATCAGTTGCACAAGTTCTTGAAACTCTA 45

CAGTGTAATAAGGAAAAATAAGTCATGCATAAAAGCAACTATAAT 90

ACATAATAGAAAATGTTATTTTCAAGCCGATGTGTAGGTTATGTG 135

TGTTCGAGAGAGAGAGAGAGAAGACAGATTACTTTCTGCTAGGGT 180

TCAAGAATGCCTTCCTGTTGGCTAAGGAAATATTTTCCTTAAGTG 225

GCTAAAAAGCTGTGTTTCAAAATATTCTTTTGATGTCTCACAAAT 270

TCAGTGGAATTCTCTTAGGTCTAAAAATATACATCTCTCTCACTT 315

TAACTTGGTGTGCTATTGTAGATTATTGGATTAAAGCACTGCTCA 360

GGGATTATGCTGCTTCTTGCCAAGCAGTCTACATTTAAAGTAGAA 405

ATAAGATGTTTCTTTTGGTGCCATAAGGTATACATTTTATGCATT 450

CTCTAGTTTTTAGAAGATACCCTAAGGGCTAAGTCTTTAACATGC 495

TGCTACAAGTTTATTCCTAATTGCCATTGGGAAATTGGCTGAAGA 540

AAGTTTTTAACAAAAGTTAACAATATTGTCATTGAGAGAATAATT 585

CAAAATGGATTTTAACTAAAAGCTTTTAAAAACTTTGGTGAGCAT 630

AGCTTGAATGCGTAATATTTAATTGCATTTAAGCCAATAACATAT 675

FIG.15B CONT.'

```
ATTAGACTGGTCTTTTTGTGCATCAAGGCATTAGATGTTAAAAGT    720

TTGAATGATTACAGATCTTAACTGATGATCACCAAGCAATTTTTC    765

             -20                            -10
             ThrTrpIleLeuThrCysIleTyrLeuGlnLe
TGTTTTCATTTAGACTTGGATTCTCACTTGCATTTATCTTCAGCT    810

                                   1
uLeuLeuPheAsnProLeuValLysThrGluGlyIleCysArgAs
GCTCCTATTTAATCCTCTCGTCAAAACTGAAGGATCTGCAGGAA     855

        10                    18
nArgValThrAsnAsnValLysAspValThrLysLeu
TCGTGTGACTAATAATGTAAAAGACGTCACTAAATTGGTAAGTAA    900

GGAATGCTTTACCGTGCTGTGTAAAAAAGAGCTGTGGCTCTTTTT    945

CCTGTGCTTGTTGATAAAAGATTTAGATTTTTCTTGCCCCAAAGT    990

AATGTTTTCCTAAAGTGGGGAAAGTAATCACTGGGTTACAATAAA    1035

GGGTTTATAGAAAGCAGGTAGTGAGATATTTAGGGTCATGGATAA    1080

TTTGTTGGTAAAACTGGCTAGTTGCACACCACTGCTGTGACTGCT    1125

TCTTTGCTGGTCTTCTCCCCATCCTTCATAGGCAGTGAAGGACCT    1170

TGGAGAGTTCGCTGTGTGCTGATGGGCTTGCCCCAGCTTGTTCCC    1215

CATAATCTCTCCAGTGGGTTTCCCAGCATGTTCTATTCCCCTTCA    1260

CATGTCTTCCTACTCTTCTTTAAAAAGCCTAACGAAAGGAAATCT    1305

GAAATGGCTATTCTCCCAATTCAATCAGCAGGAAGACCCTGTCAC    1350

ATGTCAGTGGGTGTTTGCTCCTTCAGGGAACATAGAGAGGTGATT    1395

CATTGCCCACATGTTGAAGGGACTCATCTCCCTGGTTTGTCACAT    1440

TGAACTCTTCCCTCAGCGAAAGCATTTGCATTGCTTCCC          1479
```

FIG.15B CONT.'

Intervening sequence of unknown length

```
GAATTCCAAGATCACAGGTGGAAGCTGAAATTCAGATCATGTTTC    45

CAAAACTCAGTAGGTTATACCTAGCCAGGCATAACTGAATTTGGA    90

GTCTAAAAGATCTGTATTATCACTTTTTATTTTGAAGGATGCCT    135

TTTGATTACAGAGGGAAATCAAGGATTAAAAATCAATATACATGT    180

AAATATTGAAATTCATTGGTAACTTTAAAAAGCACAACAGTTTTG    225

TGTGCTTTTCTCCAAAGCACTACAAATATGATTAATTGATGTATA    270

                                          19
                                         ValAlaA
AGAATTTTCTTATGGAATTTTTTTTTTGTCTCTGTAGGTGGCAA    315

                         30
snLeuProLysAspTyrMetIleThrLeuLysTyrValProGlyM
ATCTTCCAAAAGACTACATGATAACCCTCAAATATGTCCCCGGGA    360

       39
etAspValLeu
TGGATGTTTTGGTATGTAAACTACATTTCTGAGTTTCATTTTAGT    405

AGCTCATAGAAGAAATGGGATCATTCATATTGAGATAGTACACTA    450

GCTGCTATTTAGGAGCTTGCTTATTGTCAGGATTTGAAGAATTTA    495

TCTTTGGAATTTGACTTGCAGGCTTTTTTTTCCCCCTCTT    535
```

Intervening sequence of unknown length

```
CCTGTTACAAGAGTCCCTCCTCCTATTACAATAGTCCCTCCTCCT    45

CCTGTCACACTAGTCCCTTCTCTTCCTGTTACAATAACCCCTGTC    90
```

FIG.15B CONT.'

```
CTCCTATTACAACATTTTAAGTAATGTAATATTAATTTTAAAAAT    135

CTGGCCAGGCACGGTGGTTCATGCTTGTAATCCCAGCACATTGGG    180

AAGCTGAGACGGGTGGATCATTTGAGGTCAGGAAGTTTGAGACAG    225

CCTGGCCAACATGGTGAAACTTCCTCTCTACTAAAAATAAAAAAG    270

TAGCCAGGCATGGTGGCAGGCACTTGTAATCTGAGCTACTCGAGA    315

GGCTGAGGCAGGAGAATCACTTGAGTAACTAAAACGATAGCTTTG    360

AAGAGTACTCCGAGTTTTATGGCACTTACTTATTAAAATAGCTGT    405

                                 40
                              ProSerHisCysTrpIleS
TTTGTCTCTTTTTTCATATCTTGCAGCCAAGTCATTGTTGGATAA    450

              50                                60
erGluMetValValGlnLeuSerAspSerLeuThrAspLeuLeuA
GCGAGATGGTAGTACAATTGTCAGACAGCTTGACTGATCTTCTGG    495

                                 70
spLysPheSerAsnIleSerGluGlyLeuSerAsnTyrSerIleI
ACAAGTTTTCAAATATTTCTGAAGGCTTGAGTAATTATTCCATCA    540

              80                                90
leAspLysLeuValAsnIleValAspAspLeuValGluCysValL
TAGACAAACTTGTGAATATAGTGGATGACCTTGTGGAGTGCGTGA    585

                 96
ysGluAsnSerSerLys
AAGAAAACTCATCTAAGGTAACTTTGTGTTCATTGGGATTATTTT    630

TCATTACGCTTCTCTAAAAACCCATGCTTCTTGGTGCTGTTGGGG    675

AAAATGAGGCACCTTTATTTATGATATTTTGATTGTATAAACTTC    720

AAATTTAAAAATCTTGTTCAGATGAGCAAAGAAAACAAGTATTTG    765

CAGTTATACTGCAATACTGAAGTGCACATTC   796
```

FIG.15B CONT.'

Intervening sequence of unknown length

```
TTGTGTTCACTGCCCCAGATTCAACTTGTGATCCCACTGGGATCA   45

CTACCCTGCATTACCAATCTGAATTACATACGTTAAAACAGCCAT   90

CTAAAAGTGCTAGTTGTAAGAGTCTAAATACTTGAATCTTTGAGA   135

GACATATTTATAGTCCATTATCTTCACCTCAGTTAAGTCTGAAGA   180

                                        97
                                      AspLeuLysL
CTATTTGAAAAATGTAATCCTATTTTTTCTTCTAGGATCTAAAAA   225

                        110
ysSerPheLysSerProGluProArgLeuPheThrProGluGluP
AATCATTCAAGAGCCCAGAACCCAGGCTCTTTACTCCTGAAGAAT   270

          120                                130
hePheArgIlePheAsnArgSerIleAspAlaPheLysAspPheV
TCTTTAGAATTTTTAATAGATCCATTGATGCCTTCAAGGACTTTG   315

                          140
alValAlaSerGluThrSerAspCysValValSerSerThrLeuS
TAGTGGCATCTGAAACTAGTGATTGTGTGGTTTCTTCAACATTAA   360

     148
erProGluLysA
GTCCTGAGAAAGGTAAGACATGTAAGCATTTCCAGTTCAAATGTA   405

AACAACAAACTTAAATCTTCCCTATGTAGTAAGAATCTACCTCTG   450

TGTTAAGCTGTAGCAAGATACATGCATGTACGTCTAATAAAAAAG   495

CAGATATCAATAGCACAGAAGAAA                        519
```

Intervening sequence of unknown length

FIG.15B CONT.'

```
CTCTATAACTCATACAAATCACCATATAACACTGACACATTATTG     45

                150                                 160
              spSerArgValSerValThrLysProPheMetL
CTTTCTATTTAGATTCCAGAGTCAGTGTCACAAAACCATTTATGT     90

                                  170
euProProValAlaAlaSerSerLeuArgAsnAspSerSerSerS
TACCCCCTGTTGCAGCCAGCTCCCTTAGGAATGACAGCAGTAGCA    135

  176
erAsnA
GTAATAGTAAGTACATATATCTGATTTAATGCATGCATGGCTCCA    180

ATTAGCACCTATAGGAGTATTGCATGGGCTTTCAAGGAAACTTCT    225

ACATTTATTATTATTGATACTGTTCTGTTACTGTTATTCCTTTTA    270

TGGTCTTCTTGAGACTTAAGTTTGTAGAATTAAATTTCCCTAGAG    315

CTGGAGATAATGTTTAGAGAATTAGGCCAATAAATTT            352
```

FIG.15C

```
          -25       -20
           M  K  K  T  Q  T  W  I  L  T  C  I  Y  L  Q
AAGCTTGCCTTTCCTTATGAAGAAGACACAAACTTGGATTCTCACTTGCATTTATCTTCAG    61

-10                       1                          10
 L  L  L  F  N  P  L  V  K  T  E  G  I  C  R  N  R  V  T  N
CTGCTCCTATTTAATCCTCTCGTCAAAACTGAAGGGATCTGCAGGAATCGTGTGACTAAT   121

                         20                          30
 N  V  K  D  V  T  K  L  V  A  N  L  P  K  D  Y  M  I  T  L
AATGTAAAAGACGTCACTAAATTGGTGGCAAATCTTCCAAAAGACTACATGATAACCCTC   181

                         40                          50
 K  Y  V  P  G  M  D  V  L  P  S  H  C  W  I  S  E  M  V  V
AAATATGTCCCCGGGATGGATGTTTTGCCAAGTCATTGTTGGATAAGCGAGATGGTAGTA   241

                         60                          70
 Q  L  S  D  S  L  T  D  L  L  D  K  F  S  N  I  S  E  G  L
CAATTGTCAGACAGCTTGACTGATCTTCTGGACAAGTTTTCAAATATTTCTGAAGGCTTG   301

                         80                          90
 S  N  Y  S  I  I  D  K  L  V  N  I  V  D  D  L  V  E  C  V
AGTAATTATTCCATCATAGACAAACTTGTGAATATAGTGGATGACCTTGTGGAGTGCGTG   361

                        100                         110
 K  E  N  S  S  K  D  L  K  K  S  F  K  S  P  E  P  R  L  F
AAAGAAAACTCATCTAAGGATCTAAAAAAATCATTCAAGAGCCCAGAACCCAGGCTCTTT   421
```

FIG.15C CONT.'

```
                                    120                                130
 T  P  E  E  F  F  R  I  F  N  R  S  I  D  A  F  K  D  F  V
ACTCCTGAAGAATTCTTTAGAATTTTTAATAGATCCATTGATGCCTTCAAGGACTTTGTA   481

                                    140                                150
 V  A  S  E  T  S  D  C  V  V  S  S  T  L  S  P  E  K  D  S
GTGGCATCTGAAACTAGTGATTGTGTGGTTTCTTCAACATTAAGTCCTGAGAAAGATTCC   541

                                    160                                170
 R  V  S  V  T  K  P  F  M  L  P  P  V  A  A  S  S  L  R  N
AGAGTCAGTGTCACAAAACCATTTATGTTACCCCCTGTTGCAGCCAGCTCCCTTAGGAAT   601

                                    180      183
 D  S  S  S  S  N  S  K  Y  I  Y  L  I
GACAGCAGTAGCAGTAATAGTAAGTACATATATCTGATTTAATGCATGCATGGCTCCAAT   661

TAGCACCTATAGGAGTATTGCATGGGCTTTCAAGGAAACTTCTACATTTATTATTATTGA   721

TACTGTTCTGTTACTGTTATTCCTTTTATGGTCTTCTTGAGACTTAAGTTTGTAGAATTA   781

AATTTCCCTAGAGCTGGAGATAATGTTTAGAGAATTAGG                        820
```

GAGCTCCGAGCcCTCtCTGGCGCgCgAGGTATTTCGTCTGTnCCCGGGGGTGCCAGGTGA 60

GCCCCAGCGGATCCGGGAGGGTAAGCTGGGACTCCTCGCGAGCAGTAGCTGCAGGGTACC 120

AAGCTTCGCCCTCTGCGTCCCCGCGCCTTCGCGGTCTCCCGCCAGTGCAGGTCCGGGGCC 180

CCCAGGCGAGCGGACAAGGTTGGCCTAATCTGCCAAACTTCTGGGGCATTTACCGTGCTC 240

TGGCCGCCCTCCCGATTCTTCCCTCCGCGCCCTTGCCTGCTTCTCGCCTACCCCGGGCTC 300

CGGAAGGGAAGGAGGCGTGTCCGGAGCAGGCGGGCGGGAACTGTATAAAAGCGCCGGCGG 360

CTCAGCAGCCGGCTTCGCTCGCCGCCTCGCGCCGAGACTAGAAGCGCTGCGGGAAGCAGG 420

GACAGTGGAGAGGGCGCTGCGCTCGGGCTACCCAATGCGTGGACTATCTGCCGCCGCTGT 480

TCGTGCAATCACCCTGGAGCTCCAGAACAGCTAAACGGAGTCGCCACACCACTGTTTGTGC 540

-25 -21
MetLysLysThrGln
TGGATCGCCAGGCTGCCTTTCCTTATGAAGAAGACACAAGTGAGTAGGGCGCGCCCGGGA 600

GCTCCCAGGCTCTCCAGGAAAAATCGCGCCCGGTGCCCCGGGGAAGCCGGCGCTCCCTGG 660

GACTTGCAGCTGGGGCGTGCAGGGCTGTGCCTGCCGGGTGAGACAAGAGGATGCGGGGGA 720

GGCCGGCGTGGTGTGTGATCCCGAGCCGAGCCGnnTGAGCCAGGGAGAAAAGGAGTGGGA 780

GTnCTGAGAGGGAGCCAGTGTCAAGTTTGGAGCCTCAGCAGTTAAGTTTTGAGCTGTCAG 840

TCGGAAACCGTAATTCCCGTCTGGTGGAAAGATTGGCTTTTnGnCCACGGAATGTAAGTT 900

ATCAC 905

FIG. 15D

FIG. 15D CONT.

Intervening sequence of unknown length

```
AGATACTACAAAGATAAATCAGTTGCACAAGTTCTTGAAACTCTACAGTGTAATAAGGAA    60

AAATAAGTCATGCATAAAAGCAACTATAATACATAATAGAAAATGTTATTTTCAAGCCGA   120

TGTGTAGGTTATGTGTGTTCGAGAGAGAGAGAGAGAAGACAGATTACTTTCTGCTAGGGT   180

TCAAGAATGCCTTCCTGTTGGCTAAGGAAATATTTTCCTTAAGTGGCTAAAAAGCTGTGT   240

TTCAAAATATTCTTTTGATGTCTCACAAATTCAGTGGAATTCTCTTAGGTCTAAAAATAT   300

ACATCTCTCTCACTTTAACTTGGTGTGCTATTGTAGATTATTGGATTAAAGCACTGCTCA   360

GGGATTATGCTGCTTCTTGCCAAGCAGTCTACATTTAAAGTAGAAATAAGATGTTTCTTT   420

TGGTGCCATAAGGTATACATTTTATGCATTCTCTAGTTTTTAGAAGATACCCTAAGGGCT   480

AAGTCTTTAAGATGCTGCTACAAGTTTATTCCTAATTGCCATTGGGAAATTGGCTGAAGA   540

AAGTTTTTAAGAAAAGTTAACAATATTGTCATTGAGAGAATAATTCAAAATGGATTTTAA   600

CTAAAAGCTTTTAAAAACTTTGGTGAGCATAGCTTGAATGCGTAATATTTAATTGCATTT   660

AAGCCAATAACATATATTAGACTGGTCTTTTTGTGCATCAAGGCATTAGATGTTAAAAGT   720

                                                         -20
                                                          Th
TTGAATGATTACAGATCTTAACTGATGATCACCAAGCAATTTTTCTGTTTTCATTTAGAC   780

                      -10
rTrpIleLeuThrCysIleTyrLeuGlnLeuLeuLeuPheAsnProLeuValLysThrGl
TTGGATTCTCACTTGCATTTATCTTCAGCTGCTCCTATTTAATCCTCTCGTCAAAACTGA   840
```

```
1                                    10                                  18
uGlyIleCysArgAsnArgValThrAsnAsnValLysAspValThrLysLeu
AGGGATCTGCAGGAATCGTGTGACTAATAATGTAAAAGACGTCACTAAATTGGTAAGTAA     900

GGAATGCTTTACCGTGCTGTGTAAAAAAGAGCTGTGGCTCTTTTTCCTGTGCTTGTTGAT     960

AAAAGATTTAGATTTTTCTTGCCCCAAAGTAATGTTTTCCTAAAGTGGGGAAAGTAATCA     1020

CTGGGTTACAATAAAGGGTTTATAGAAAGCAGGTAGTGAGATATTTAGGGTCATGGATAA     1080

TTTGTTGGTAAAACTGGCTAGTTGCACACCACTGCTGTGACTGCTTCTTTGCTGGTCTTC     1140

TCCCCATCCTTCATAGGCAGTGAAGGACCTTGGAGAGTTCGCTGTGTGCTGATGGGCTTG     1200

CCCCAGCTTGTTCCCCATAATCTCTCCAGTGGGTTTCCCAGCATGTTCTATTCCCCTTCA     1260

CATGTCTTCCTACTCTTCTTTAAAAAGCCTAACGAAAGGAAATCTGAAATGGCTATTCTC     1320

CCAATTCAATGAGCAGGAAGACCCTGTCACATGTCAGTGGGTGTTTGCTCCTTCAGGGAA     1380

CATAGAGAGGTGATTCATTGCCCACATGTTGAAGGGACTCATCTCCCTGGTTTGTCACAT     1440

TGAACTCTTCCCTCAGCGAAAGCATTTGCATTGCTTCCC                          1479
```

Intervening sequence of unknown length

```
GAATTCCAAGATCACAGGTGGAAGGTGAAATTCAGATCATGTTTCCAAAACTCAGTAGGT     60

TATACCTAGCCAGGCATAACTGAATTTGGAGTCTAAAAGATCTGTATTATCACTTTTTTA     120

TTTTGAAGGATGCCTTTTGATTACAGAGGGAAATCAAGGATTAAAAATCAATATACATGT     180
```

FIG. 15D CONT.

AAATATTGAAATTCATTGGTAACTTTAAAAAGCACAACAGTTTTGTGTGCTTTTCTCCAA 240

AGCACTACAAATATGATTAATTGATGTATAAGAATTTTCTTATGGAATTTTTTTTTTTGT 300

19 30
ValAlaAsnLeuProLysAspTyrMetIleThrLeuLysTyrValProGlyM
CTCTGTAGGTGGCAAATCTTCCAAAAGACTACATGATAACCCTCAAATATGTCCCCGGGA 360

39
etAspValLeu
TGGATGTTTTGGTATGTAAACTACATTTCTGAGTTTCATTTTAGTAGCTCATAGAAGAAA 420

TGGGATCATTCATATTGAGATAGTACACTAGCTGCTATTTAGGAGCTTGCTTATTGTCAG 480

GATTTGAAGAATTTATCTTTGGAATTTGACTTGCAGGCTTTTTTTTCCCCCTCTT 535

Intervening sequence of unknown length

CCTGTTACAAGAGTCCCTCCTCCTATTACAATAGTCCCTCCTCCTCCTGTCACACTAGTC 60

CCTTCTCTTCCTGTTACAATAACCCCTGTCCTCCTATTACAACATTTTAAGTAATGTAAT 120

ATTAATTTTAAAAATCTGGCCAGGCACGGTGGTTCATGCTTGTAATCCCAGCACATTGGG 180

AAGCTGAGACGGGTGGATCATTTGAGGTCAGGAAGTTTGAGACAGCCTGGCCAACATGGT 240

GAAACTTCCTCTCTACTAAAAATAAAAAAGTAGCCAGGCATGGTGGCAGGCACTTGTAAT 300

CTGAGCTACTCGAGAGGCTGAGGCAGGAGAATCACTTGAGTAACTAAAACGATAGCTTTG 360

AAGAGTACTCCGAGTTTTATGGCACTTACTTATTAAAATAGCTGTTTTGTCTCTTTTTTC 420

FIG. 15D CONT.

FIG. 15D CONT.

```
              40                                 50
             ProSerHisCysTrpIleSerGluMetValValGlnLeuSerAspSerL
ATATCTTGCAGCCAAGTCATTGTTGGATAAGCGAGATGGTAGTACAATTGTCAGACAGCT    480

              60                                 70
euThrAspLeuLeuAspLysPheSerAsnIleSerGluGlyLeuSerAsnTyrSerIleI
TGACTGATCTTCTGGACAAGTTTTCAAATATTTCTGAAGGCTTGAGTAATTATTCCATCA    540

              80                                 90
leAspLysLeuValAsnIleValAspAspLeuValGluCysValLysGluAsnSerSerL
TAGACAAACTTGTGAATATAGTGGATGACCTTGTGGAGTGCGTGAAAGAAAACTCATCTA    600
96
ys
AGGTAACTTTGTGTTCATTGGGATTATTTTTCATTACGCTTCTCTAAAAACCCATGCTTC    660

TTGGTGCTGTTGGGGAAAATGAGGCACCTTTATTTATGATATTTTGATTGTATAAACTTC    720

AAATTTAAAAATCTTGTTCAGATGAGCAAAGAAAACAAGTATTTGCAGTTATACTGCAAT    780

ACTGAAGTGCACATTC                                                796


                Intervening sequence of unknown length


TTGTGTTCACTGCCCCAGATTCAACTTGTGATCCCACTGGGATCACTACCCTGCATTACC    60

AATCTGAATTACATACGTTAAAACAGCCATCTAAAAGTGCTAGTTGTAAGAGTCTAAATA    120

CTTGAATCTTTGAGAGACATATTTATAGTCCATTATCTTCACCTCAGTTAAGTCTGAAGA    180

                                       97
                                      AspLeuLysLysSerPheLysSerP
CTATTTGAAAAATGTAATCCTATTTTTCTTCTAGGATCTAAAAAAATCATTCAAGAGCC     240
```

```
                110                                          120
roGluProArgLeuPheThrProGluGluPhePheArgIlePheAsnArgSerIleAspA
CAGAACCCAGGCTCTTTACTCCTGAAGAATTCTTTAGAATTTTTAATAGATCCATTGATG    300

                130                                          140
laPheLysAspPheValValAlaSerGluThrSerAspCysValValSerSerThrLeuS
CCTTCAAGGACTTTGTAGTGGCATCTGAAACTAGTGATTGTGTGGTTTCTTCAACATTAA    360

        148
erProGluLysA
GTCCTGAGAAAGGTAAGACATGTAAGCATTTCCAGTTCAAATGTAAACAACAAACTTAAA    420

TCTTCCCTATGTAGTAAGAATCTACCTCTGTGTTAAGCTGTAGCAAGATACATGCATGTA    480

CGTCTAATAAAAAAGCAGATATCAATAGCACAGAAGAAACTAATGATTGTAGATTTGTGGG   541

                    Intervening sequence of unknown length

                                                         spS
CTCTATAACTCATACAAATCACCATATAACACTGACACATTATTGCTTTCTATTTAGATT    60

150                                 160
erArgValSerValThrLysProPheMetLeuProProValAlaAlaSerSerLeuArgA
CCAGAGTCAGTGTCACAAAACCATTTATGTTACCCCCTGTTGCAGCCAGCTCCCTTAGGA    120

170           176
snAspSerSerSerSerAsnA
ATGACAGCAGTAGCAGTAATAGTAAGTACATATATCTGATTTAATGCATGCATGGCTCCA    180

ATTAGCACCTATAGGAGTATTGCATGGGCTTTCAAGGAAACTTCTACATTTATTATTATT    240

GATACTGTTCTGTTACTGTTATTCCTTTTATGGTCTTCTTGAGACTTAAGTTTGTAGAAT    300
```

FIG. 15D CONT.

```
TAAATTTCCCTAGAGCTGGAGATAATGTTTAGAGAATTAGGCCAATAAATTTTCTGCTGA   360

GGTTATTTTAAATAAGACATAAAATTAATTTTAGAAATATGATTTATGCCTTTTGTTGAA   420

TCATTAACATATAT                                                 434


              Intervening sequence of unknown length


ACAGAAACAGTTAAAACAACCACAGCATAAGAGnAAAACTTCTAGAATGGATATGCTGTA   60

                                    178
                                rgLysAlaLysAsnProProGlyAspSerSerL
TTCATCAGTGTGTTCTTTAAATTATAGGGAAGGCCAAAAATCCCCCTGGAGACTCCAGCC   120

      190                                 200
euHisTrpAlaAlaMetAlaLeuProAlaLeuPheSerLeuIleIleGlyPheAlaPheG
TACACTGGGCAGCCATGGCATTGCCAGCATTGTTTTCTCTTATAATTGGCTTTGCTTTTG   180

               213
lyAlaLeuTyrTrpLys
GAGCCTTATACTGGAAGGTAAGTGGTACCATTCCTTtTTTTAAAAATATGCTATGTtTAC   240

ATAAATTATCATCTTTTTTTCCTCAAGAAATGATCCTTtAAGAAAACAGTGAATCTACCT   300

TAGCTTATACTAAACAAAATTTAAATTTTATAAAGTTTCCTGTTTCTCATTATGTCTGGA   360

GACAATCCCTCTAGCTGATAATTCACGCTTAAGAATTAGGAACT                   404


              Intervening sequence of unknown length
```

FIG. 15D CONT.

```
AAAACTGTTATTGGAGTTATTGCCATAAAAGATAAAAGTGGAGTCCACTTACCTCTTAAA    60
                                                      214
                                                      LysArgG
TATTAGACCATTCATTGATTATTTTACAGTATATGTCTTTCTTCTTTTTCCAGAAGAGAC   120

        220                       230         235
lnProSerLeuThrArgAlaValGluAsnIleGlnIleAsnGluGluAspAsnGluIleS
AGCCAAGTCTTACAAGGCCAGTTGAAAATATACAAATTAATGAAGAGGATAATGAGATAA   180

e
GGTATTTTGTTTTGCTAAATGTGTgCCCAATCAAGCATGACATTGCCATTTCACACACTG   240

TGTACCTGCCCATAATGTCTTTAAGAAGTCCTTCACTCATGACAGTAGCTCCTAACCAGT   300

GAGTCCCAACTCTATCCATGTTTCTGATGTCTCACTCTCTCTTC                   344

              Intervening sequence of unknown length

GTATGTGTATATGCATATACAGAGAAAGAAATGTTTTAACTACTTGGAAAGACTACCTTA    60

AGACAAATGAAGTCTTCCCTCTTCCCTATAGTAATAAGAAGGTAGGCTCCCCCATTCAAT   120

TTTGCAATCTTCTGCTACTATATTTACAGAAAAGCTGCCTTTTACAATGCCGAGATCATG   180

                                                          rM
GTGTACCTCAGAATCTCTGACCAAGAGCAAATAAGCATTTtTTCTTATTGTTTTTCAGTA   240

237                    248
etLeuGlnGluLysGluArgGluPheGlnGluVal
TGTTGCAAGAGaAAGAGAGAGAGTTTCAAGAAGTGTAATTGTGGCTTGTATCAACACTGT   300

TACTTTCGTACATTGGTAAGTTTTTTTCTTCTTTCCTTTTTTTTTCTTTTTTTTATTATA   360
```

FIG. 15D CONT.

CTTTAAGTTCTAGGGTACATGTGCACAATGTGCAGGTTTGTTACGTATGTTTACATGTGC 420

CATGTT 426

FIG. 15D CONT.

FIG.16A

```
          -25                                                     25
Human     MKKTQTWILT CIYLQLLLFN PLVKTEGICR NRVTNNVKDV TKLVANLPKD
Monkey    MKKTQTWILT CIYLQLLLFN PLVKTEGICR NRVTNNVKDV TKLVANLPKD
Dog       MKKTQTWIIT CIYLQLLLFN PLVKTKGICG KRVTDDVKDV TKLVANLPKD
Cat       MKXTQTWIVT CIYLQXLLFN PLVKTKGLCR NRVTDDVKDV TKLVANLPKD
Cow       MKKTQTWIIT CIYLQLLLFN PLVHTQGICS NRVTDDVKDV TKLVANLPKD
Rat       MKKTQTWIIT CIYLQLLLFN PLVKTQEICR NPVTDNVKDI TKLVANLPND
Mouse     MKKTQTWIIT CIYLQLLLFN PLVKTKEICG NPVTDNVKDI TKLVANLPND
Chicken        TWIIT CFCLQLLLLN PLVKAQSSCG NPVTDDVNDI AKLVGNLPND
Scfpep    MKkTQTWIiT CiyLQlLLfN PLVkt.giCr nrVTd.VkDv tKLVaNLPkD

          26                                                      72
Human     YMITLKYVPG MDVLPSHCWI SEMVVQLSDS LTDLLDKFSN ISEG...LSN
Monkey    YMITLKYVPG MDVLPSHCWI SEMVVQLSDS LTDLLDKFSN ISEG...LSN
Dog       YKIALKYVPG MDVLPSHCWI SVMVEQLSVS LTDLLDKFSN ISEG...LSN
Cat       YKIALKYVPG MDVLPSHCWI SVMVEQLSVS LTDLLDKFSN ISEG...LSN
Cow       YMITLKYVPG MDVLPSHCWI SEMVEQLSVS LTDLLDKFSN ISEG...LSN
Rat       YMITLNYVAG MDVLPSHCWL RDMVTHLSVS LTTLLDKFSN ISEG...LSN
Mouse     YMITLNYVAG MDVLPSHCWL RDMVIQLSLS LTTLLDKFSN ISEG...LSN
Chicken   YLITLKYVPK MDSLPNHCWL HLMVPEFSRS LHNLLQKFSD ISDMSDVLSN
Scfpep    YmItLkYVpg MDvLPsHCWi seMVeqlSvS LtdLLdKFSn ISeg...LSN

          73                                                      121
Human     YSIIDKLVNI VDDLVECVKE NSSKD.LKKS FKSPEPRLFT PEEFFRIFNR
Monkey    YSIIDKLVNI VDDLVECVKE NSSKD.LKKS FKSPEPRLFT PEEFFRIFNR
Dog       YSIIDKLVKI VDDLVECTEG YSFEN.VKKA PKSPELRLFT PEEFFRIFNR
Cat       YSIIDKLVKI VDDLVECVEG HSSEN.VKKS SKSPEPRLFT PEEFFRIFNR
Cow       YCIIDKLVKI VDDLVECMEX HSSEN.VKKS SKSPEPRQFT PEKFFGIFNK
Rat       YSIIDKLGKI VDDLVACMEE NAPKN.VKES LKKPETRNFT PEEFFSIFNR
Mouse     YSIIDKLGKI VDDLVLCMEE NAPKN.IKES PKKPETRSFT PEEFFSIFNR
Chicken   YSIINNLTRI INDLMACLAF DKNKDFIKEN GHLYEEDRFI PENFFRLFNS
Scfpep    YsIIdkLvkI vdDLveC.ee nsskn.vKks .kspEprlFt PEeFFriFNr
```

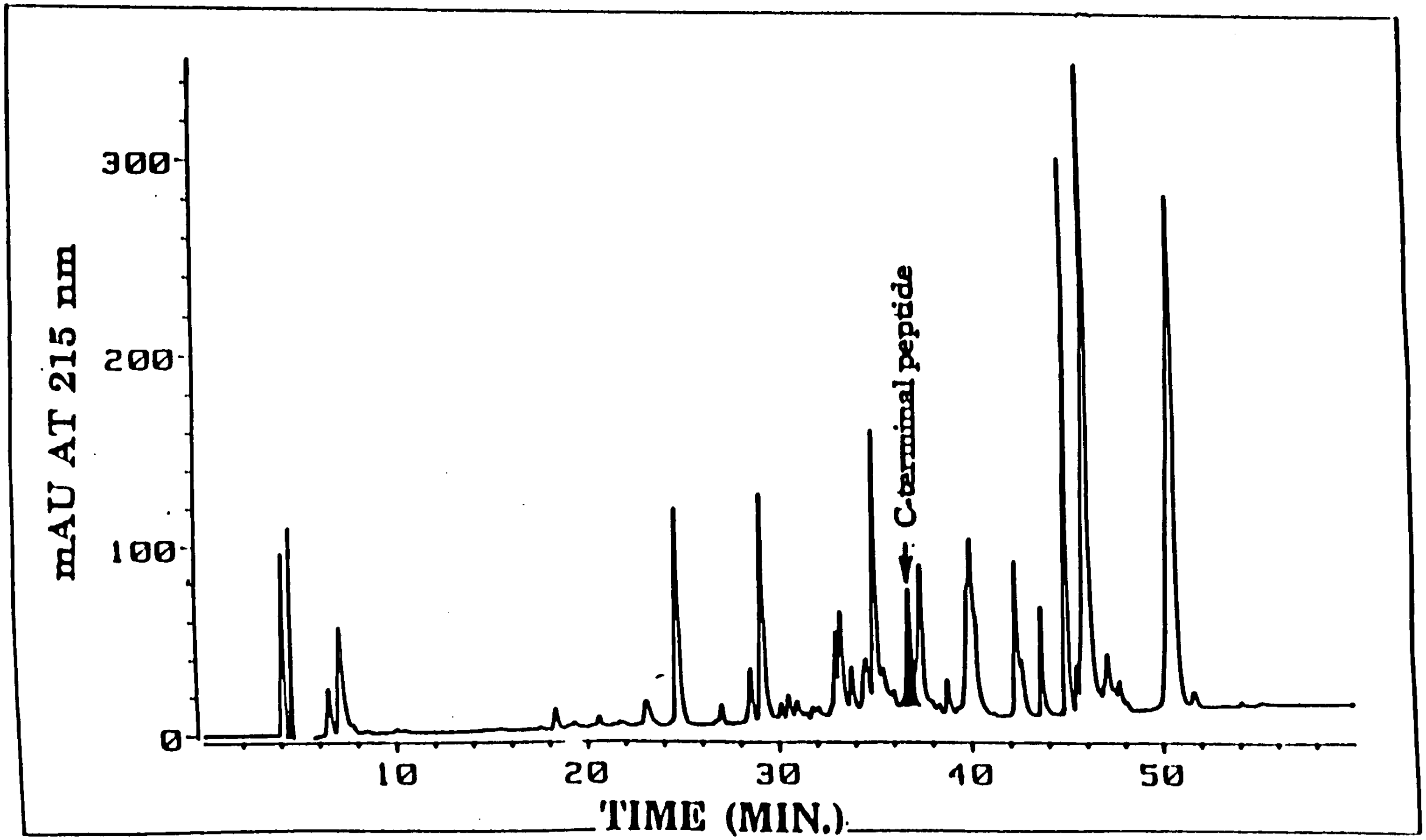
FIG.16B

```
        122                                                   169
Human   SIDAFKDF.V VASETSDCVV SSTL.SPEKD SRVSVTKPFM LPPVAASSLR
Monkey  SIDAFKDF.A VASETSDCVV SSTL.SPEKD SRVSVTKPFM LPPVAASSLR
Dog     SIDAFKDLET VASKSSECVV SSTL.SPDKD SRVSVTKPFM LPPVAASSLR
Cat     SIDAFKDLEM VASKTSECVV SSTL.SPEKD SRVSVTKPFM LPPVAASSLR
Cow     SIDAFKDLEI VASKMSECVI SSTS.SPEKD SRVSVTKPFM LPPVAASSLR
Rat     SIDAFKDF.M VASDTSDCVL SSTL.GPEKD SRVSVTKPFM LPPVAASSLR
Mouse   SIDAFKDF.M VASDTSDCVL SSTL.GPEKD SRVSVTKPFM LPPVAASSLR
Chicken TIEVYKEFAD SLDK.NDCIM PSTVETPEND SRVAVTKTIS FPPVAASSLR
Scfpep  sIdafKdf.m vasktsdCvv sSTl.sPekD SRVsVTKpfm lPPVAASSLR
```

```
        170                                                   213
Human   NDSSSSNRKA KNPPGD.... ..SSLHWAAM ALPALFSLII GFAFGALYWK
Monkey  NDSSSSNRKA KNPTGD.... ..SSLHWAAM ALPAFFSLII GFAFGALYWK
Dog     NDSSSSNRKA SNSIGD.... ..SNLQWAAM ALPAFFSLVI GFAFGALYWK
Cat     NDSSSSNRKX TNPIED.... ..SSIQWAVM ALPACFSLVI GFAFGAFYWK
Cow     NDSSSSNRKA SNSIED.... ..SSLQWAAV ALPAFFSLVI GFAFGAFYWK
Rat     NDSSSSNRKA AKSPED.... ..PGLQWTAM ALPALISLVI GFAFGALYWK
Mouse   NDSSSSNRKA AKAPED.... ..SGLQWTAM ALPALISLVI GFAFGALYWK
Chicken NDSIGSNTSS NSNKEALGFI SSSSLQGISI ALTSLLSLLI GFILGAIYWK
Scfpep  NDSssSNrka .n..ed.... ..sslqwaam ALpalfSLvI GFafGAlYWK
```

```
        214                              248
Human   KRQPSLTRAV ENIQIN...E EDNEISMLQE KEREFQEV
Monkey  KRQPSLTRAV ENIQIN...E DDNEISMLQE KEREFQEV
Dog     KKQPNLTRTV ENIQIN...E EDNEISMLQE KEREFQEV
Cat     KKQPNLTRTV ENIQIN...E EDNEISMLQE KEREFQEV
Cow     KKQPNLTRTV ENRQIN...E EDNEISMLQE KEREFQEV
Rat     KKQSSLTRAV ENIQIN...E EDNEISMLQQ KEREFQEV
Mouse   KKQSSLTRAV ENIQIN...E EDNEISMLQQ KEREFQEV
Chicken KTHPKSRPES NETIQCHGCQ EENEISMLQQ KEKEHLQV
Scfpep  Kkqpsltrav eniqin...e edNEISMLQe KErEfqeV
```

FIG. 16C



mAU AT 215 nm
300
200
100
0
C-terminal peptide
10
20
30
40
50
TIME (MIN.)

FIG. 16D

```
EcoRI
          ta  a   t   t   t a  a      t   t   c     g     t   a
GAATTCTTCCGTATCTTCAACCGTTCCATCGACGCTTTCAAAGACTTCGTT
E  F  F  R  I  F  N  R  S  I  D  A  F  K  D  F  V

  g   a   t       ta gt   t  t   g      t   a   at a ag   t   g
GTTGCTTCCGAAACCTCCGACTGCGTTGTTTCCTCCACCCTGTCTCCGGAA
V  A  S  E  T  S  D  C  V  V  S  S  T  L  S  P  E

                          BstEII
      t   a a   ca gt   c   a     a   t    t a   c   t  ·  a
AAAGACTCCCGTGTTTCGGTTACCAAACCGTTCATGCTGCCGCCGGTTGCT
K  D  S  R  V  S  V  T  K  P  F  M  L  P  P  V  A

 c ag         t a  g   t    ag  ag t ag  ag t   tag t   g     a   t
GCTTCCTCCCTGCGTAACGACTCCTCCTCCTCCAACTCCAAATACATCTAC
A  S  S  L  R  N  D  S  S  S  S  N  S  K  Y  I  Y

                 BamHI
     t
CTGATCTAATAGGATCC
L  I  •  •
```

FIG. 16E

BstEII   BamHI

GGTTACCAAACCGTTCATGCTGCCGCCGGTTGCTGCTTAATAGGATCC

V T K P F M L P P V A A • •

FIG.17

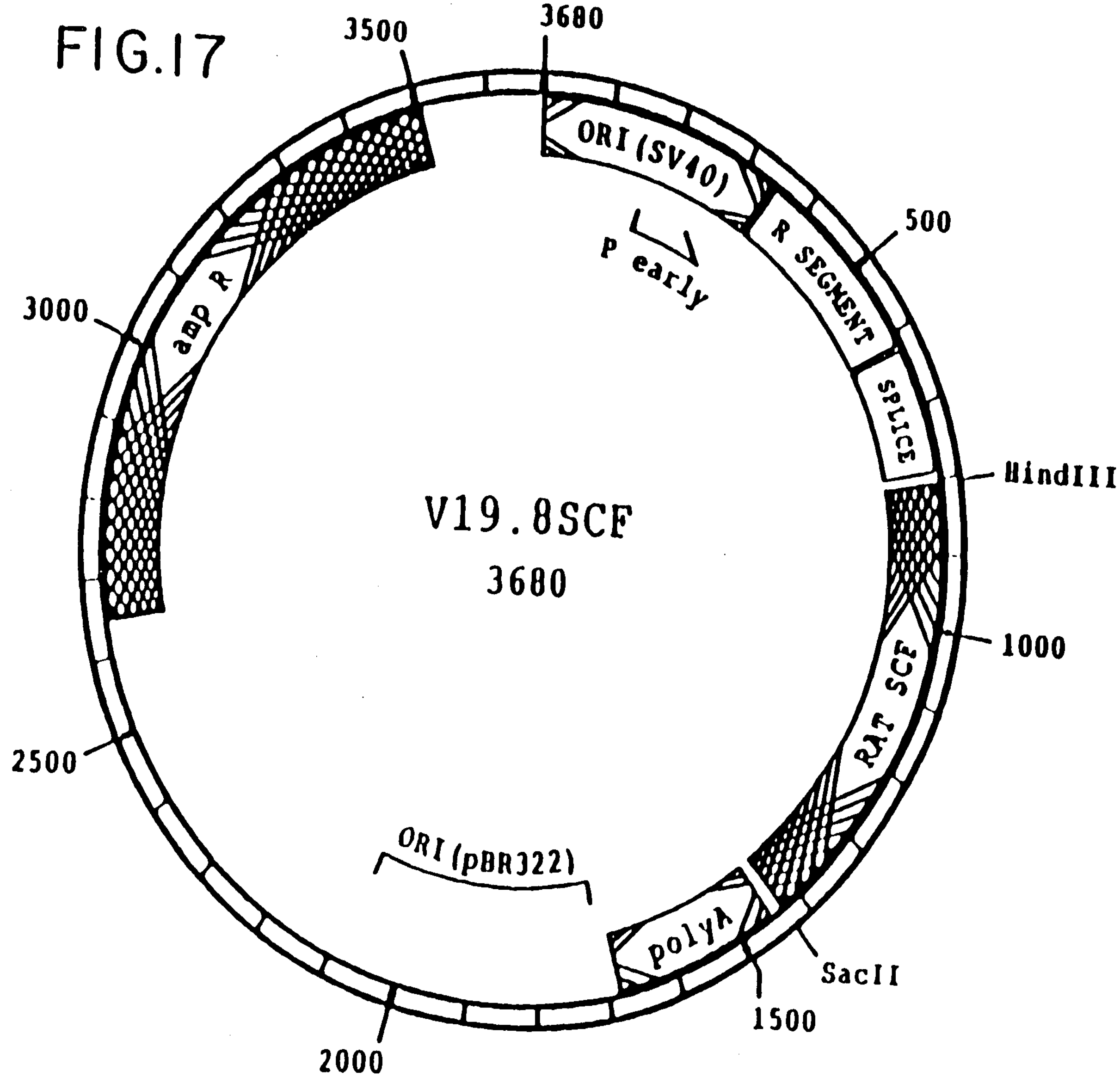

3680
3500
500
3000
2500
2000
1500
1000
HindIII
SacII
ORI (SV40)
P early
R SEGMENT
SPLICE
RAT SCF
polyA
ORI (pBR322)
amp R
V19.8SCF
3680

FIG.18

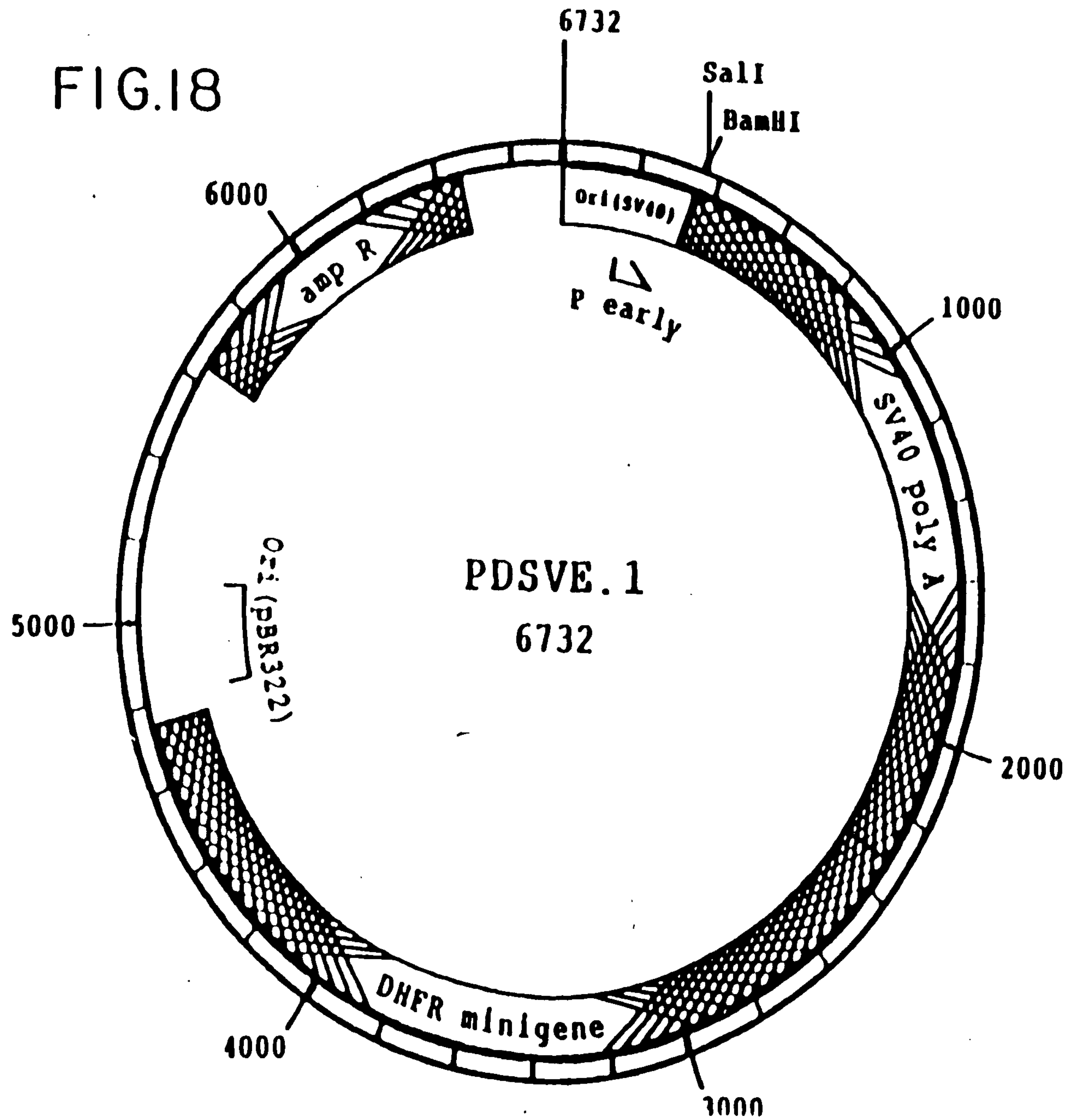
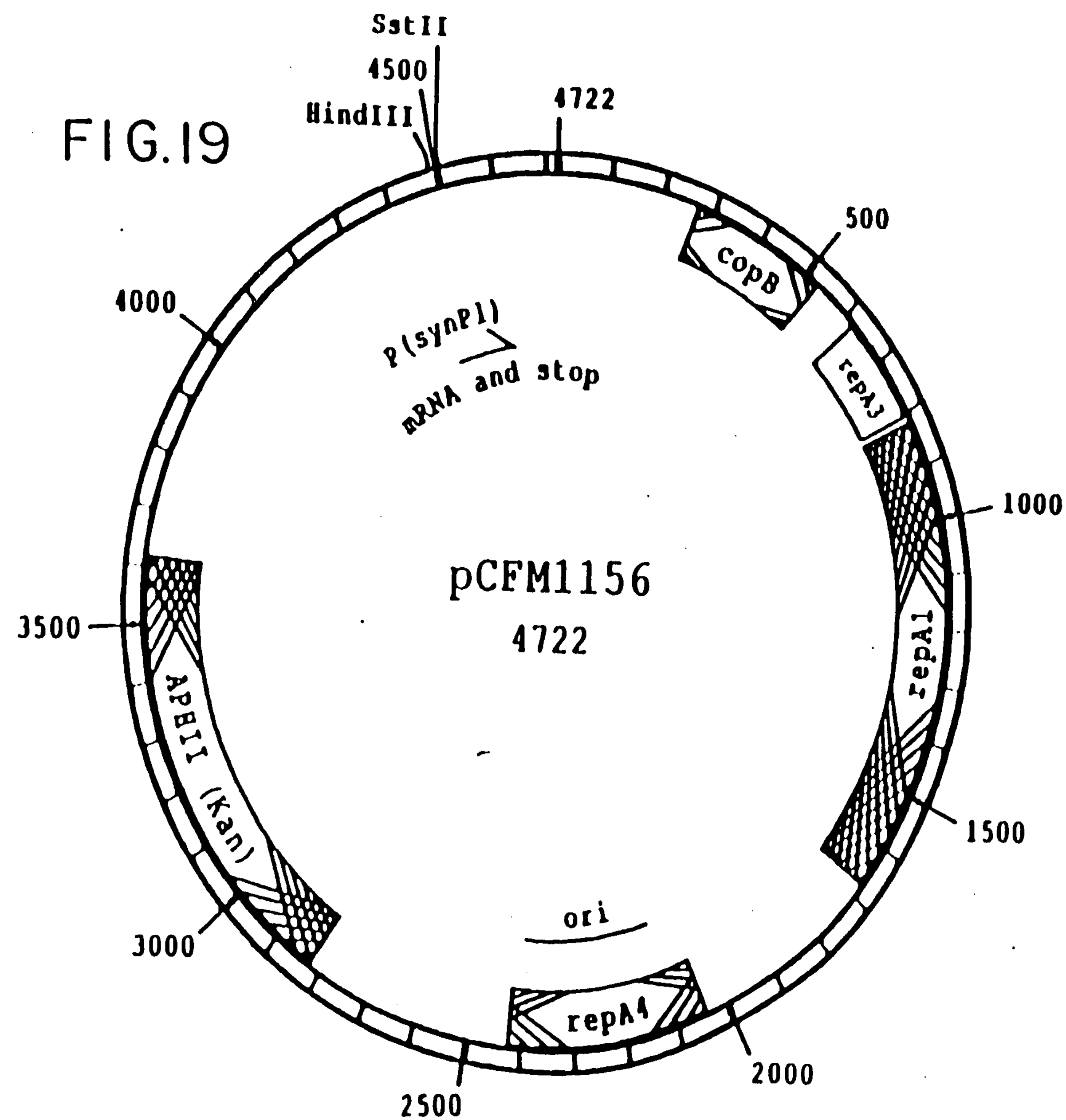
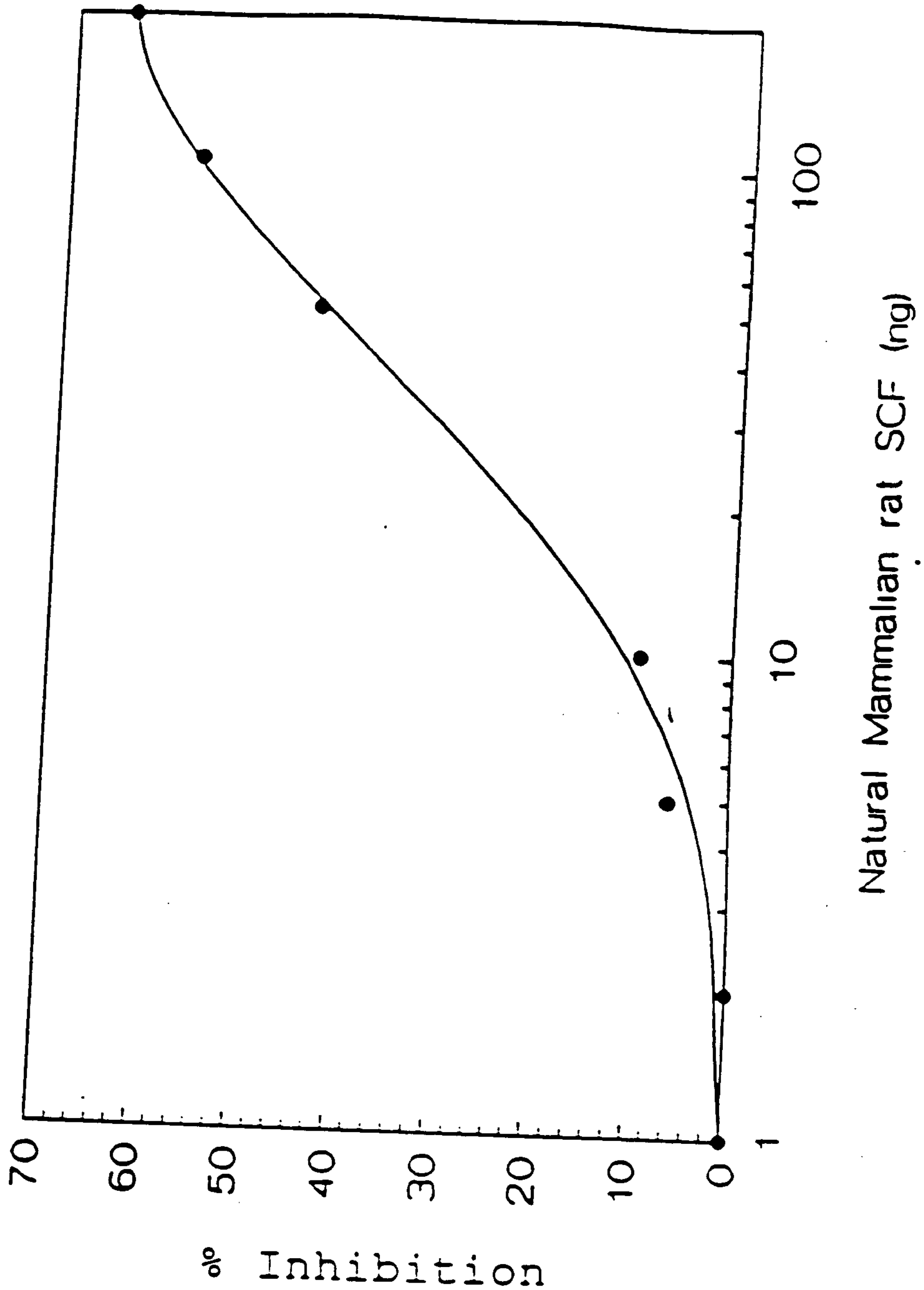

6732
SalI
BamHI
Ori(SV40)
P early
1000
SV40 poly A
2000
3000
DHFR minigene
4000
5000
Ori(pBR322)
6000
amp R
PDSVE.1
6732

FIG.19



SstII
4500
HindIII
4722
500
copB
repA3
1000
repA1
1500
2000
repA4
ori
2500
3000
APHII (Kan)
3500
4000
p(synPl)
mRNA and stop
pCFM1156
4722

FIG.20A



% Inhibition
Natural Mammalian rat SCF (ng)
0
10
20
30
40
50
60
70
1
10
100

FIG. 20B

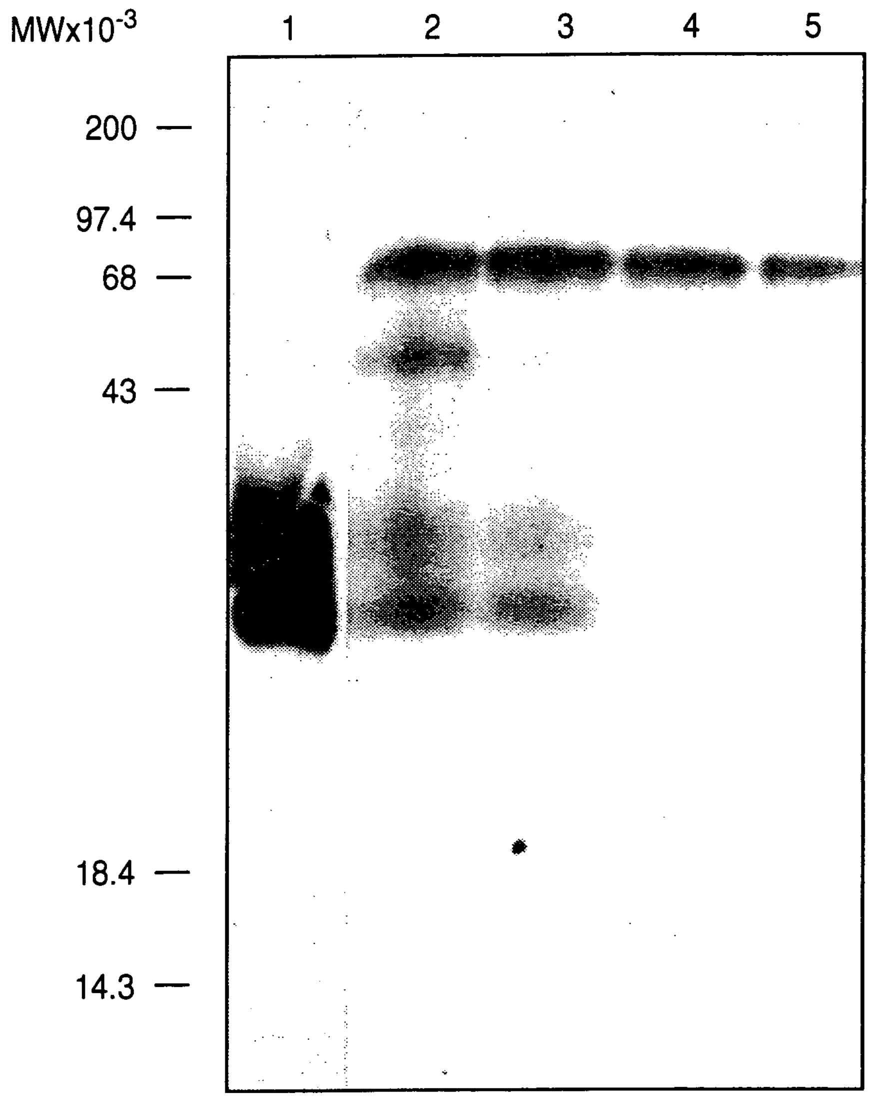


FIG. 21

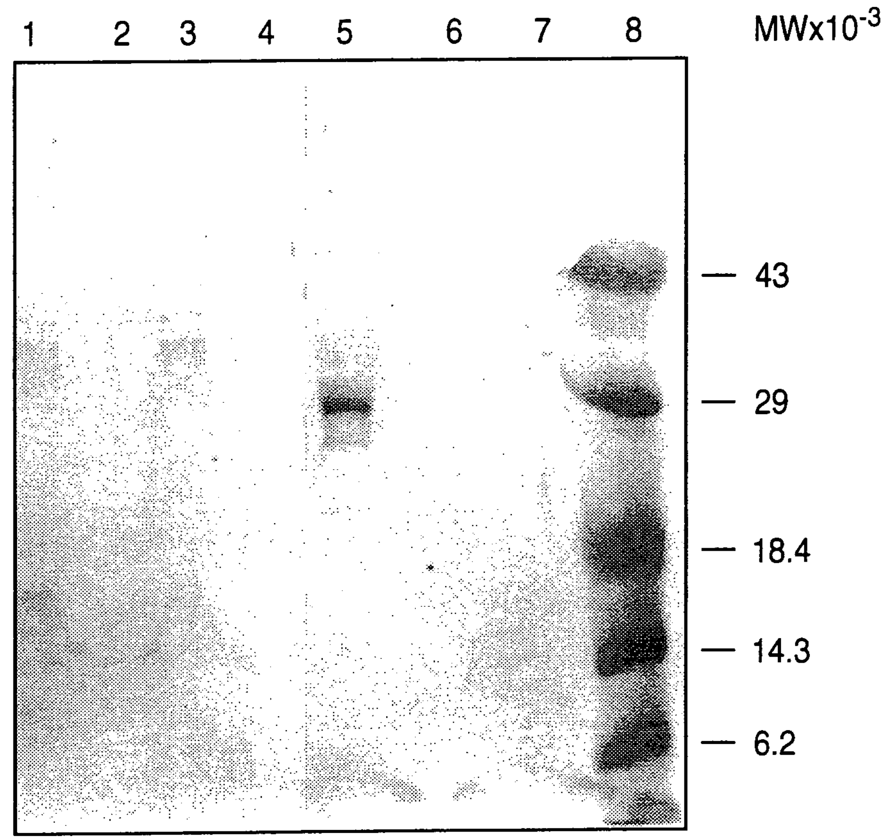


FIG. 22

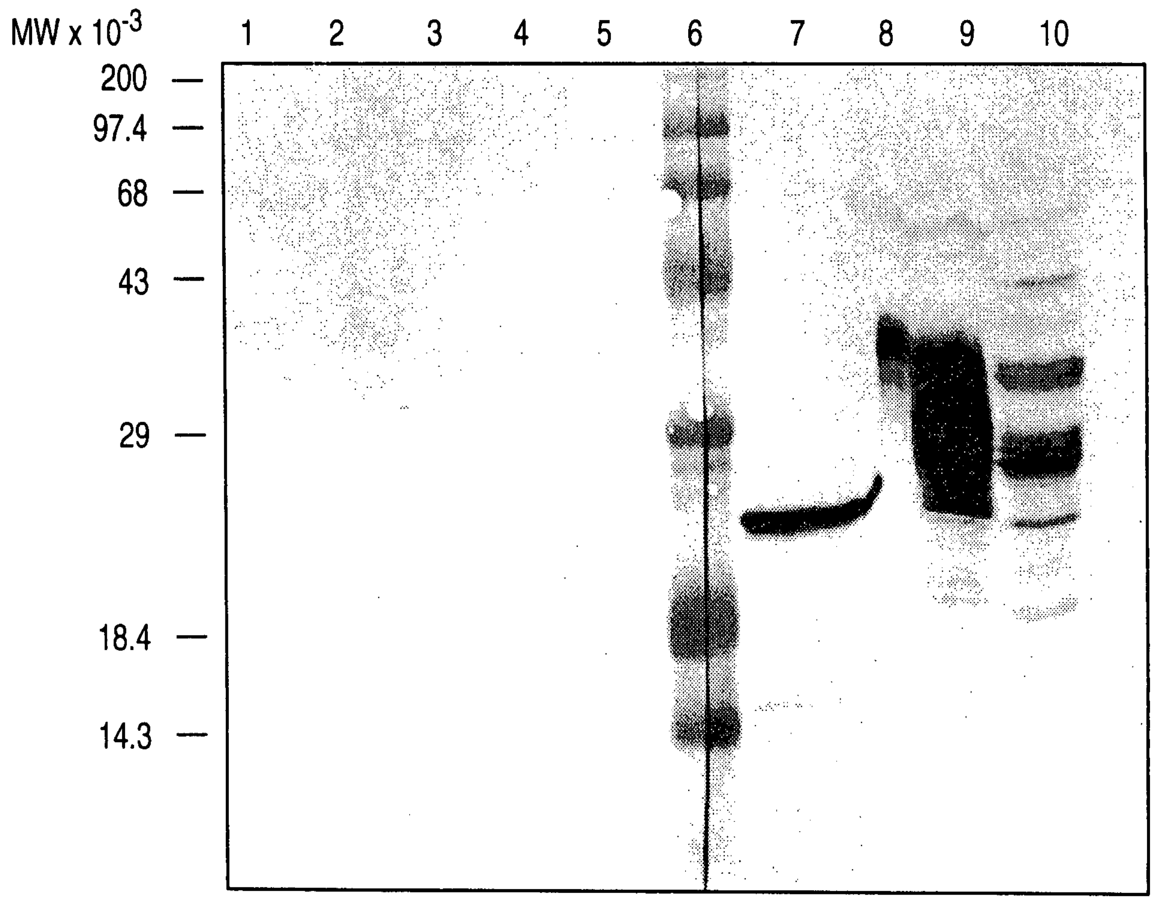


FIG. 22A

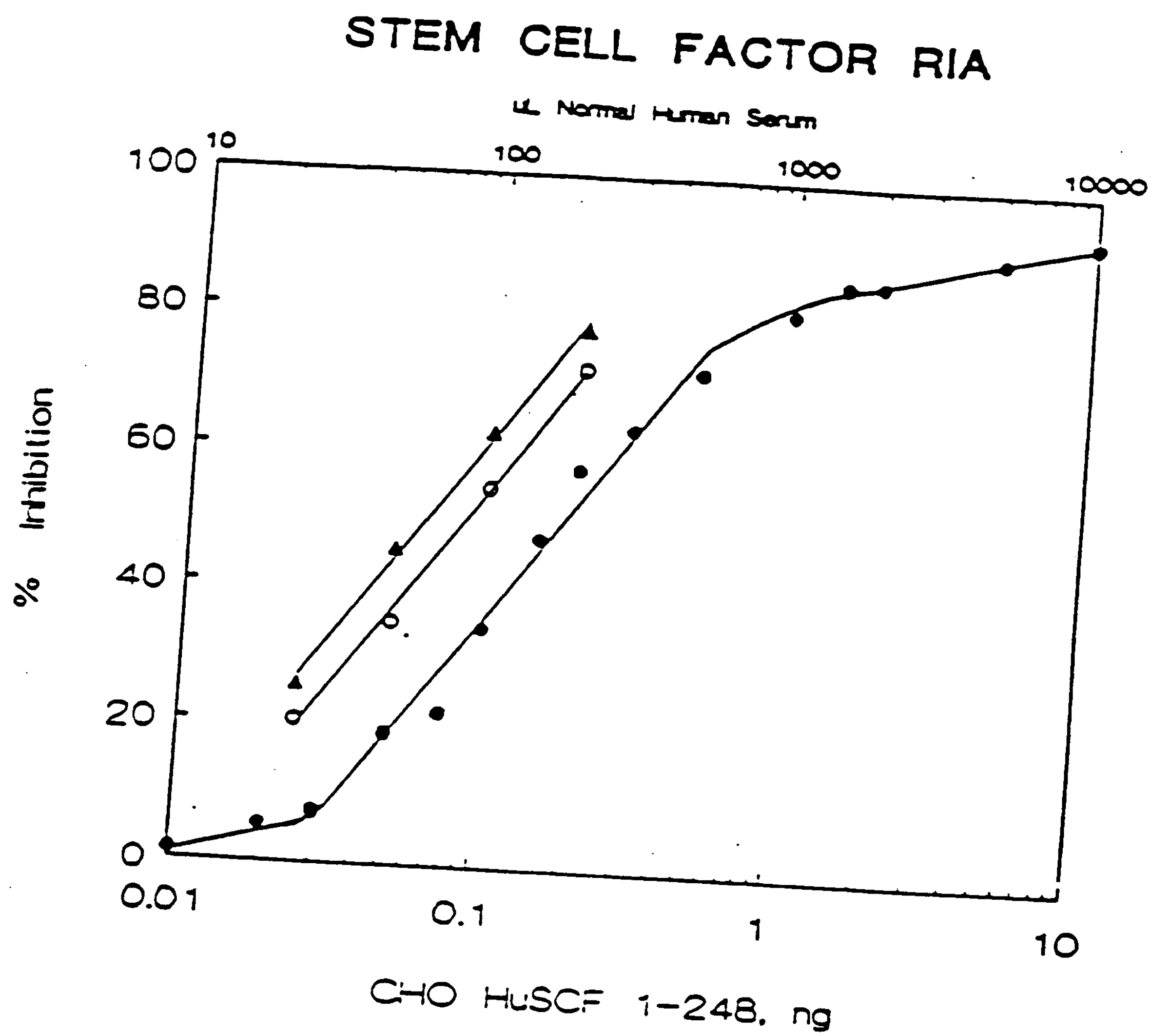
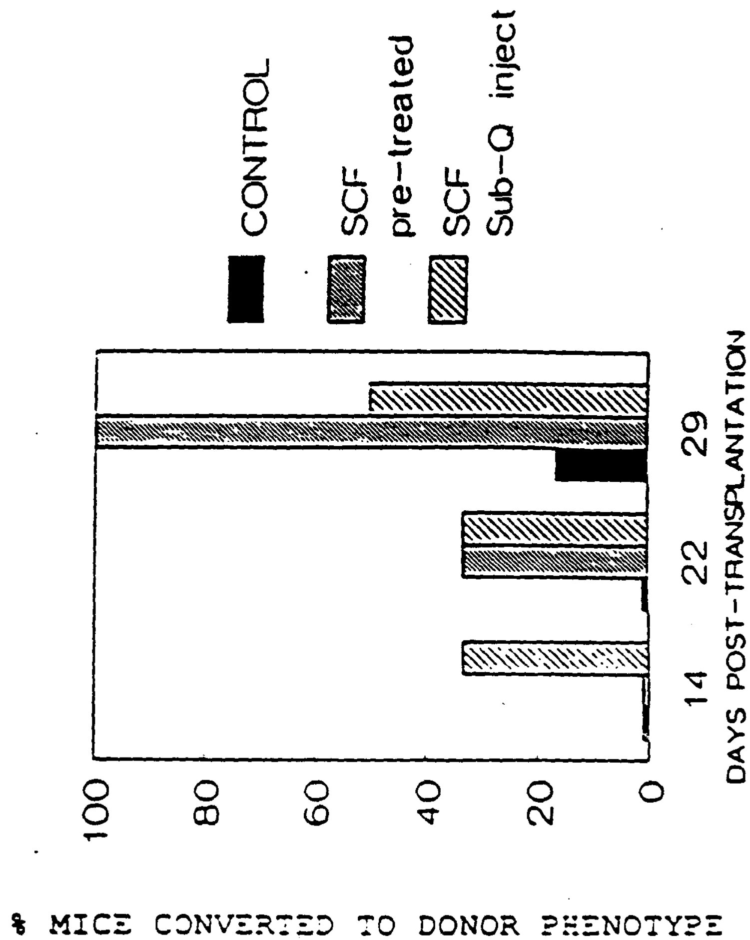

STEM CELL FACTOR RIA
uL Normal Human Serum
10
100
1000
10000
100
80
60
40
20
0
% Inhibition
0.01
0.1
1
10
CHO HuSCF 1-248, ng

FIG.23



CONTROL
SCF pre-treated
SCF Sub-Q inject
100
80
60
40
20
0
14
22
29
DAYS POST-TRANSPLANTATION
% MICE CONVERTED TO DONOR PHENOTYPE

FIG. 24A

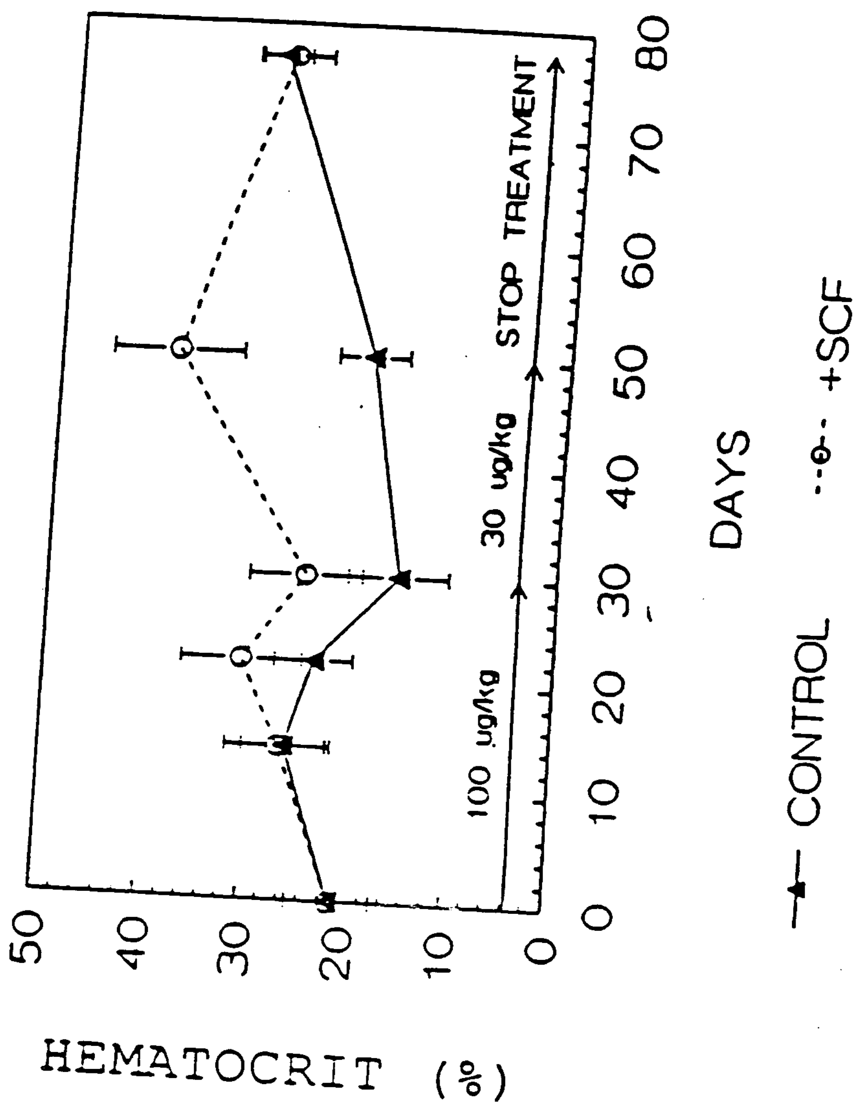
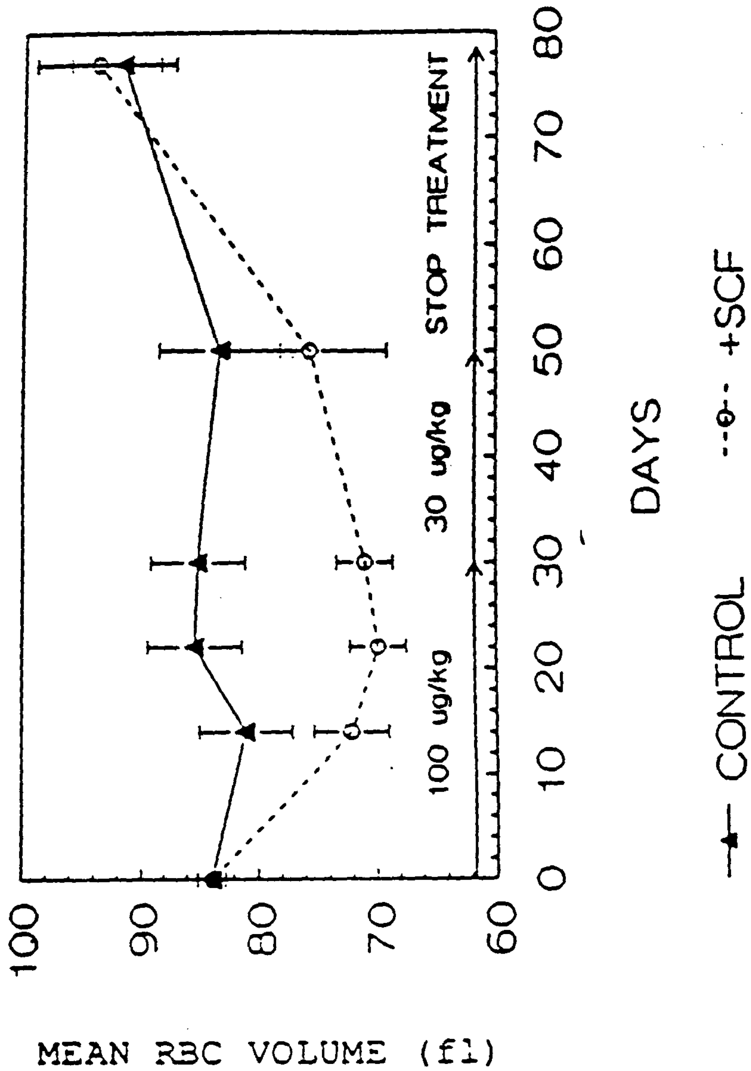
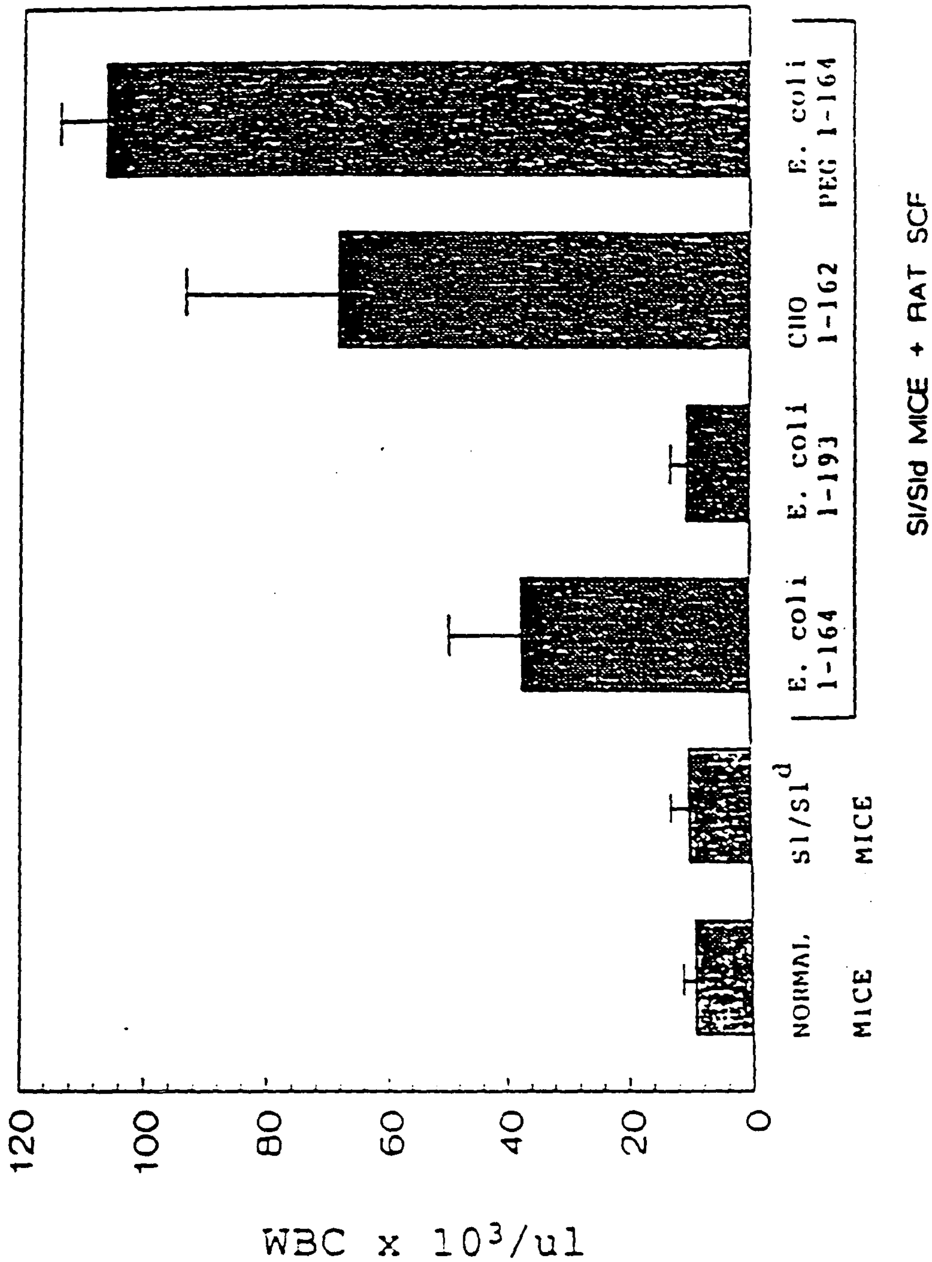

HEMATOCRIT (%)
50
40
30
20
10
0
DAYS
0
10
20
30
40
50
60
70
80
100 ug/kg
30 ug/kg
STOP TREATMENT
CONTROL
+SCF

FIG. 24B



100 ug/kg
30 ug/kg
STOP TREATMENT
0
10
20
30
40
50
60
70
80
DAYS
100
90
80
70
60
MEAN RBC VOLUME (fl)
CONTROL
+SCF

FIG.25



NORMAL MICE
Sl/Sl^d MICE
E. coli 1-164
E. coli 1-193
CHO 1-162
E. coli PEG 1-164
Sl/Sld MICE + RAT SCF
120
100
80
60
40
20
0
WBC x 10^3/ul

FIG.26

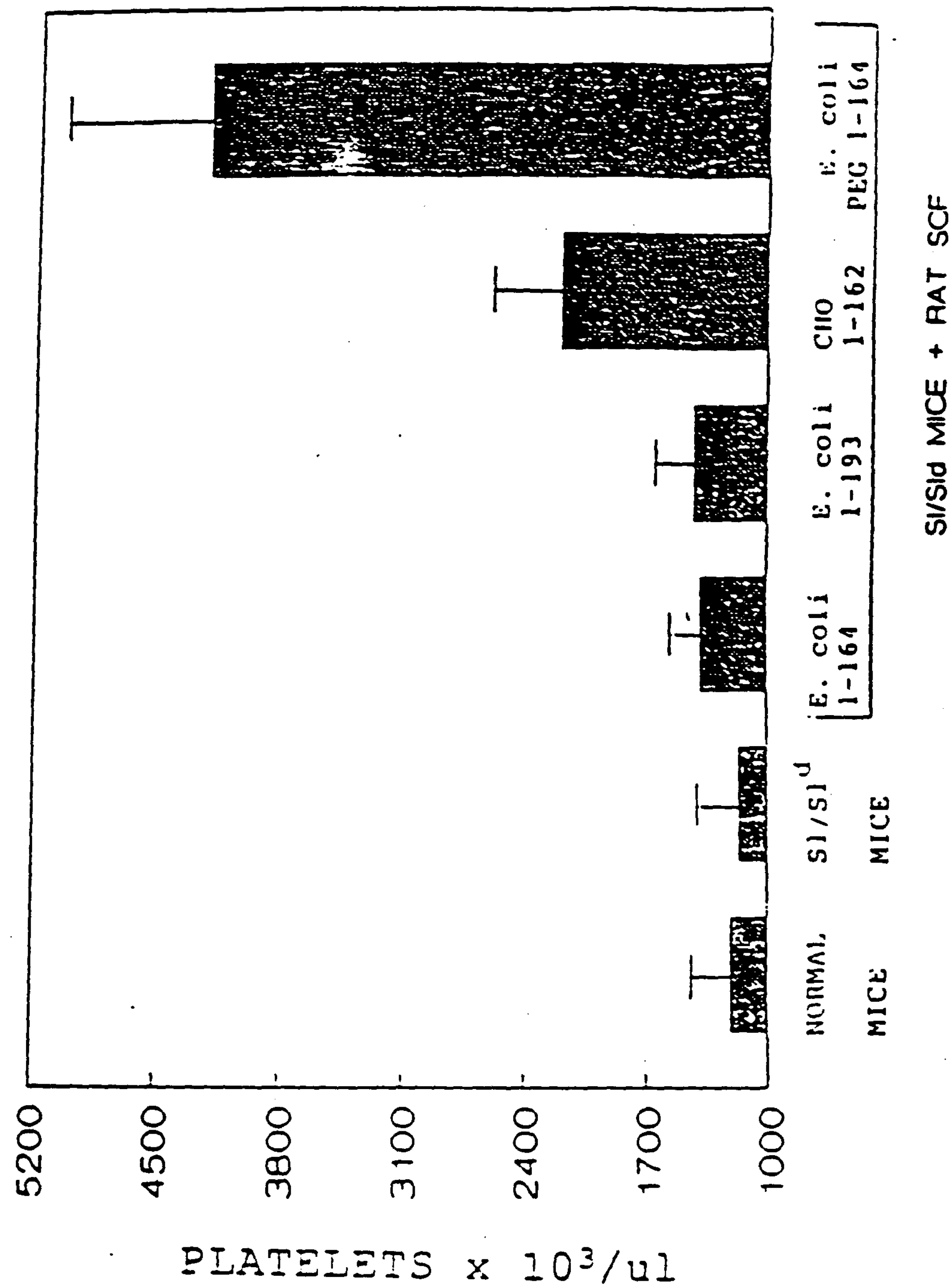

PLATELETS x 10³/ul
5200
4500
3800
3100
2400
1700
1000
NORMAL MICE
Sl/Sl^d MICE
E. coli 1-164
E. coli 1-193
CHO 1-162
E. coli PEG 1-164
Sl/Sld MICE + RAT SCF

FIG. 27

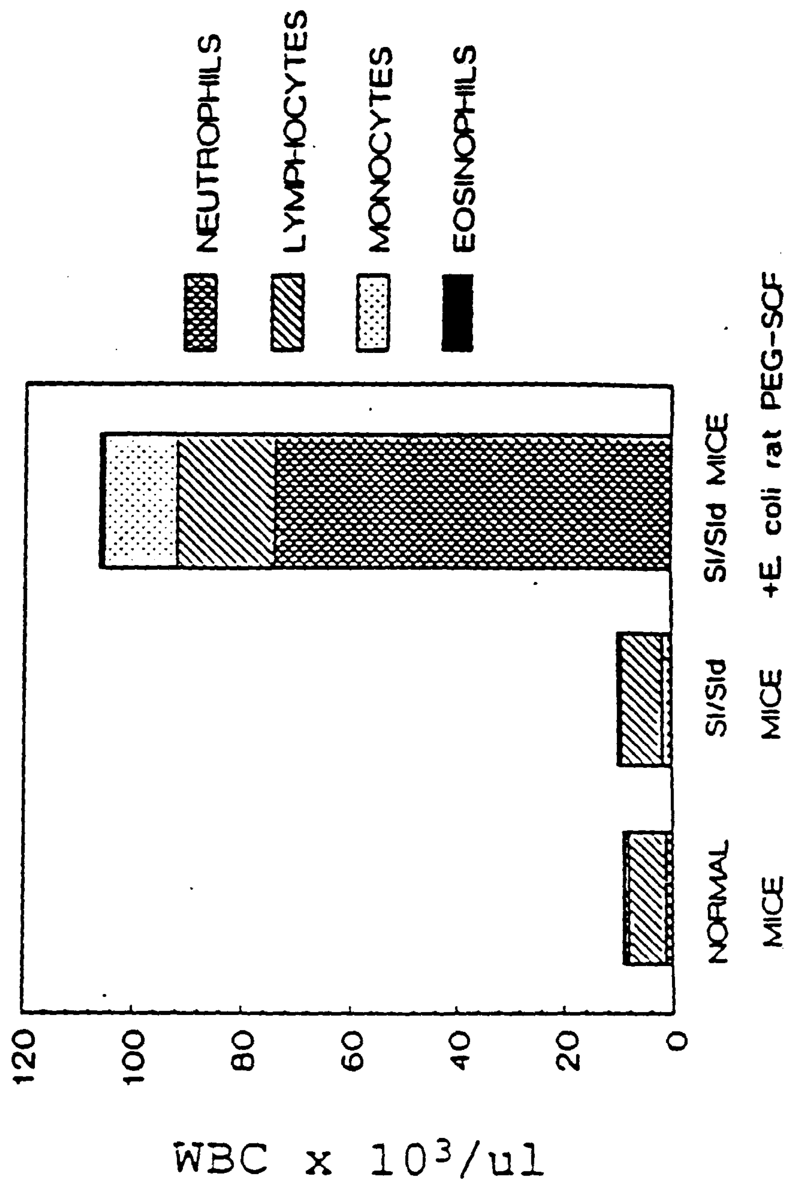
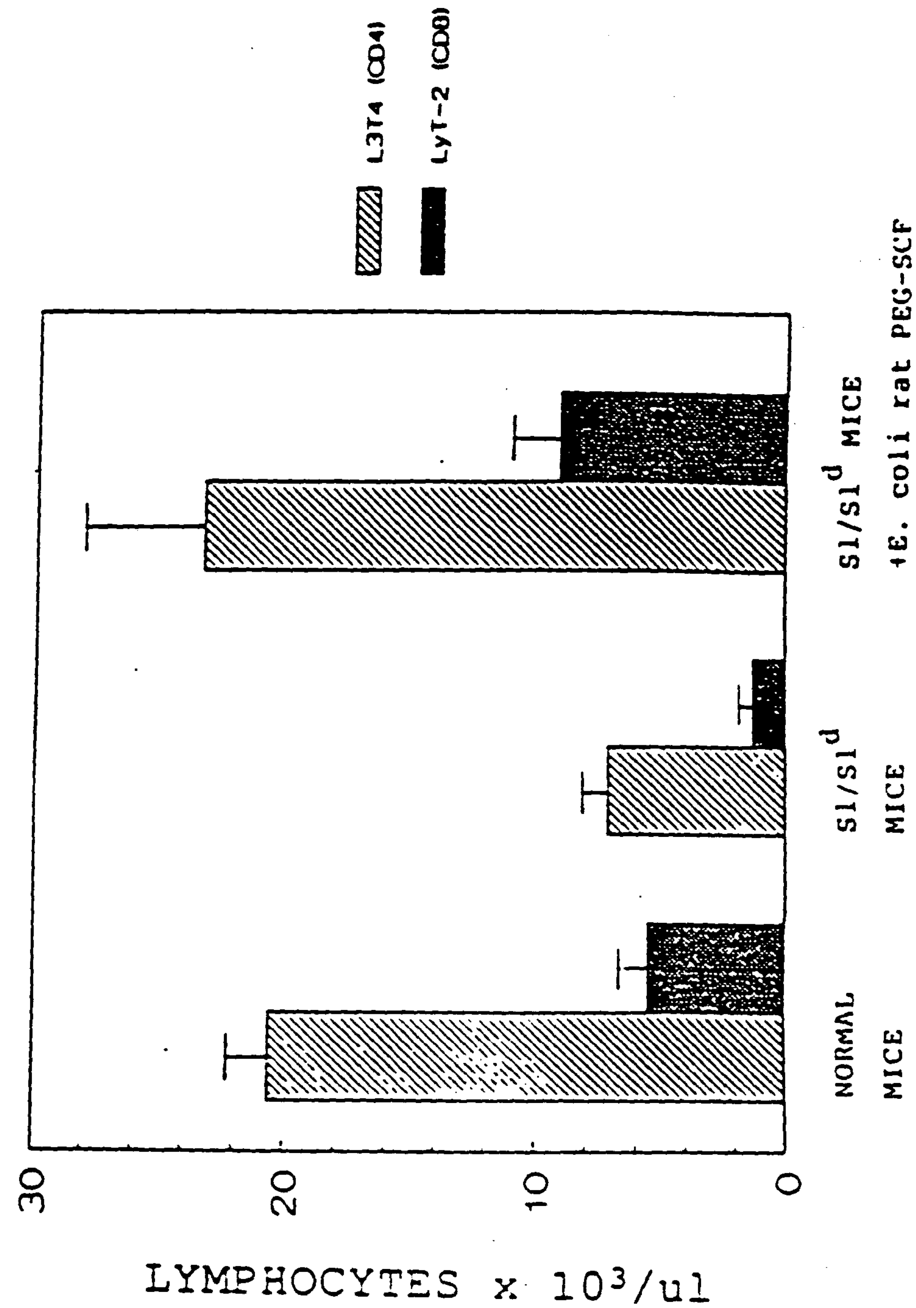

NEUTROPHILS
LYMPHOCYTES
MONOCYTES
EOSINOPHILS
120
100
80
60
40
20
0
WBC x 10³/ul
NORMAL MICE
Sl/Sld MICE
Sl/Sld MICE +E. coli rat PEG-SCF

FIG.28



L3T4 (CD4)
LyT-2 (CD8)
NORMAL MICE
Sl/Sl^d MICE
Sl/Sl^d MICE +E. coli rat PEG-SCF
0
10
20
30
LYMPHOCYTES x 10³/ul

FIG.29A

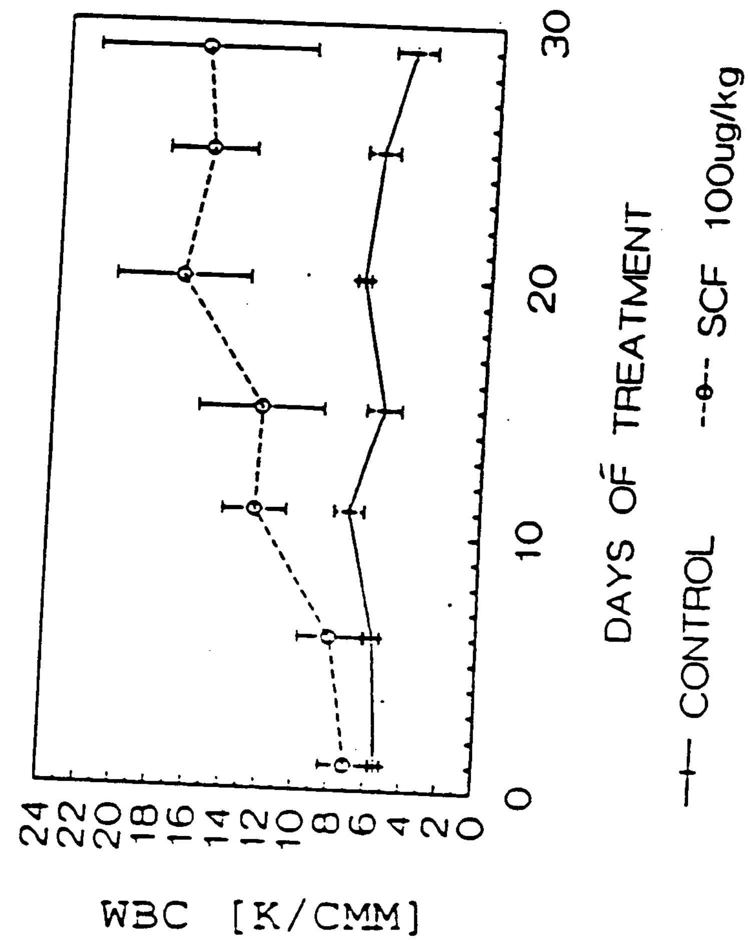

WBC [K/CMM]
0
2
4
6
8
10
12
14
16
18
20
22
24
0
10
20
30
DAYS OF TREATMENT
CONTROL
SCF 100ug/kg

FIG.29B

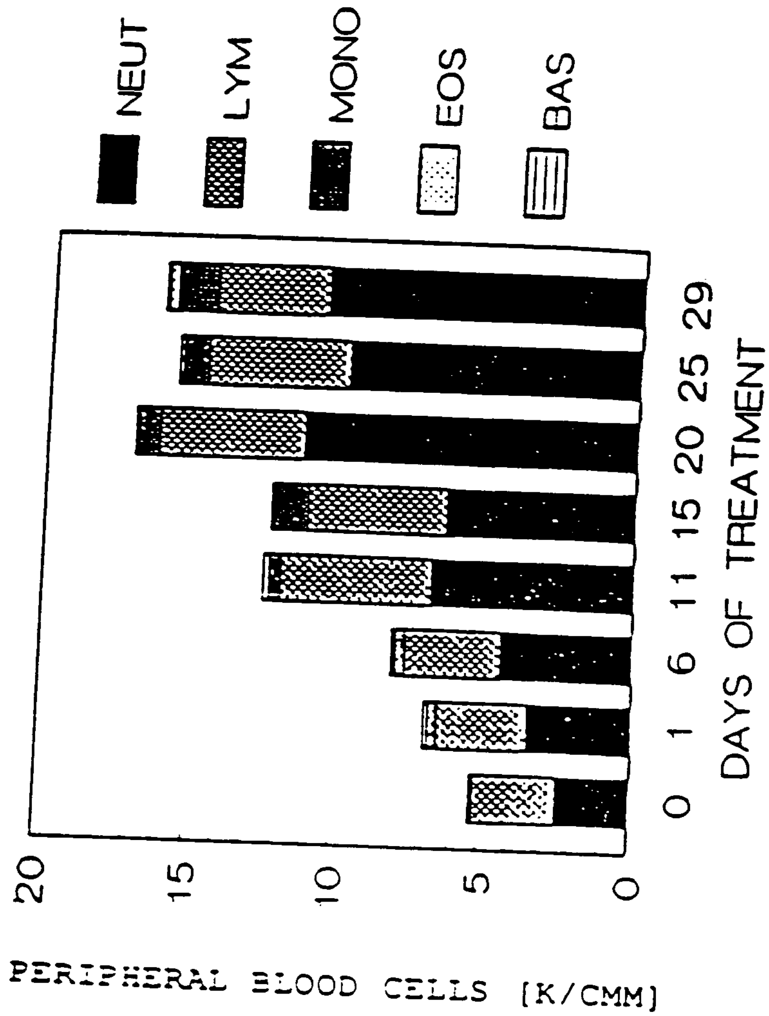
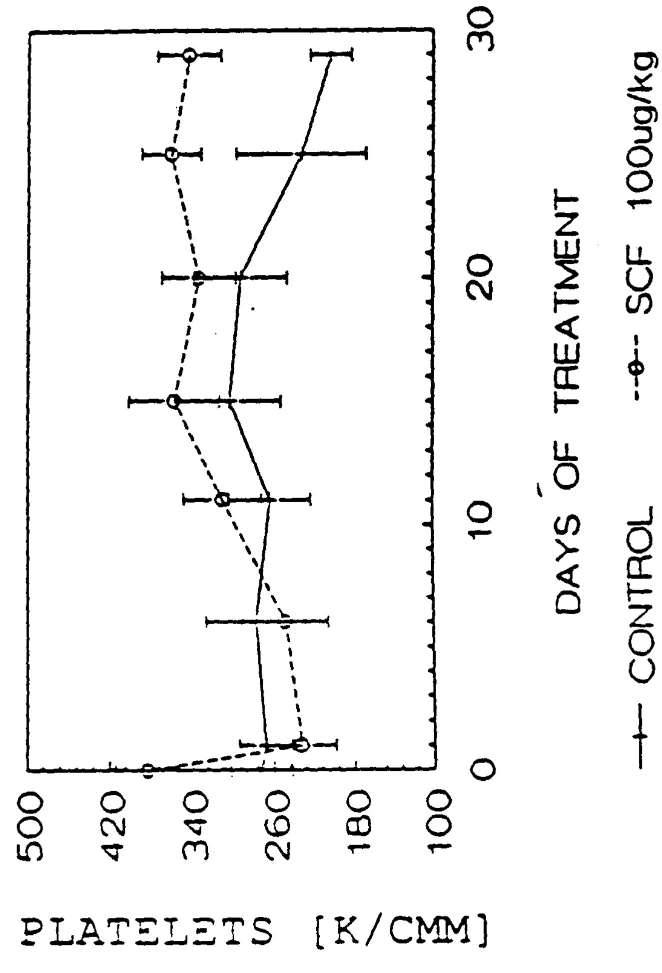
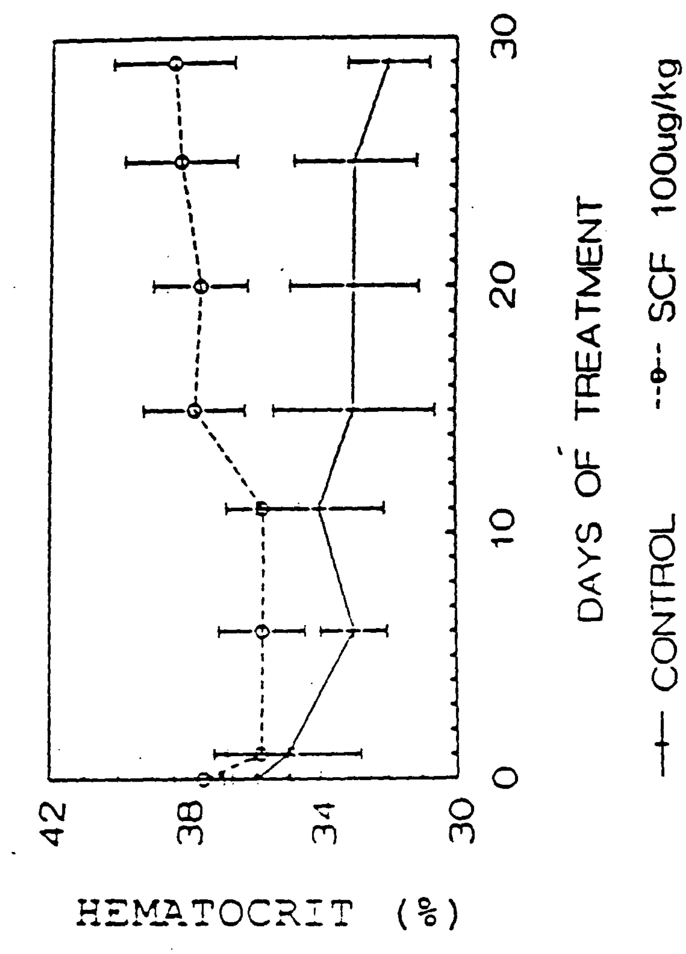

NEUT
LYM
MONO
EOS
BAS
0
5
10
15
20
0 1 6 11 15 20 25 29
DAYS OF TREATMENT
PERIPHERAL BLOOD CELLS (K/CMM)

FIG.30A



PLATELETS [K/CMM]
500
420
340
260
180
100
0
10
20
30
DAYS OF TREATMENT
CONTROL
SCF 100ug/kg

FIG.30B



HEMATOCRIT (%)
42
38
34
30
0
10
20
30
DAYS OF TREATMENT
CONTROL
SCF 100ug/kg

FIG. 31A

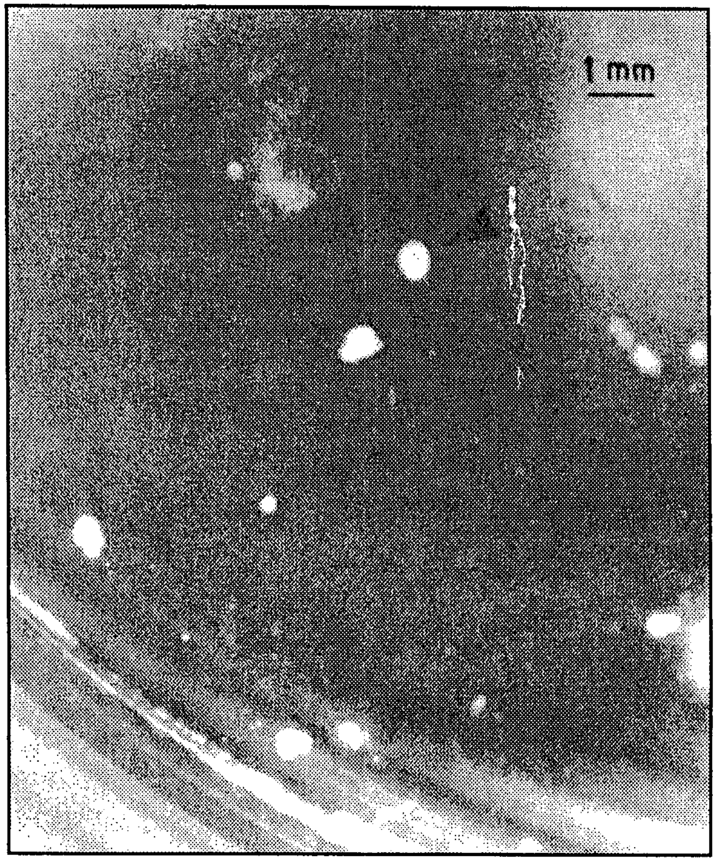


FIG. 31B

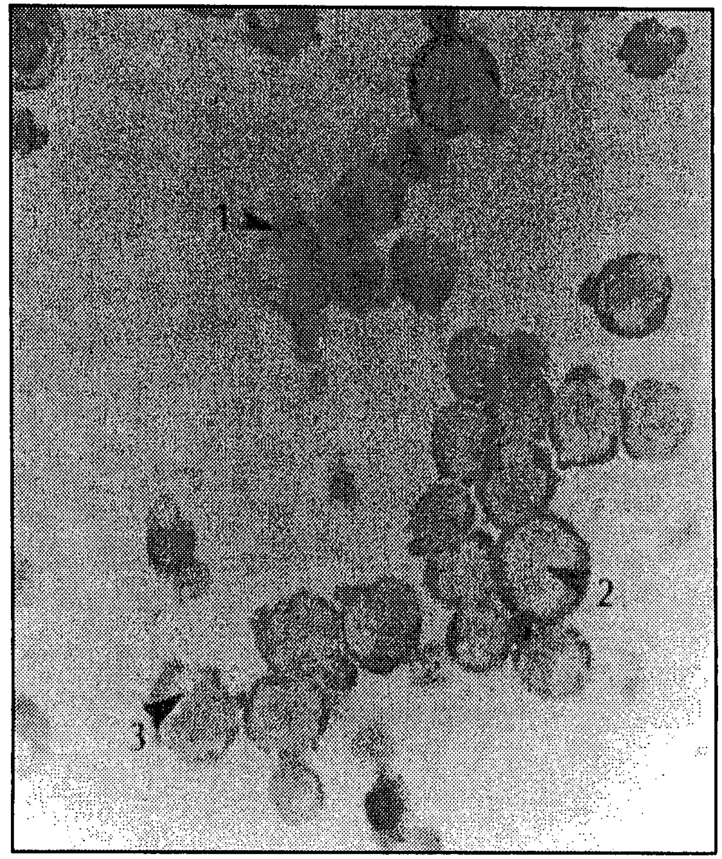


FIG. 31C

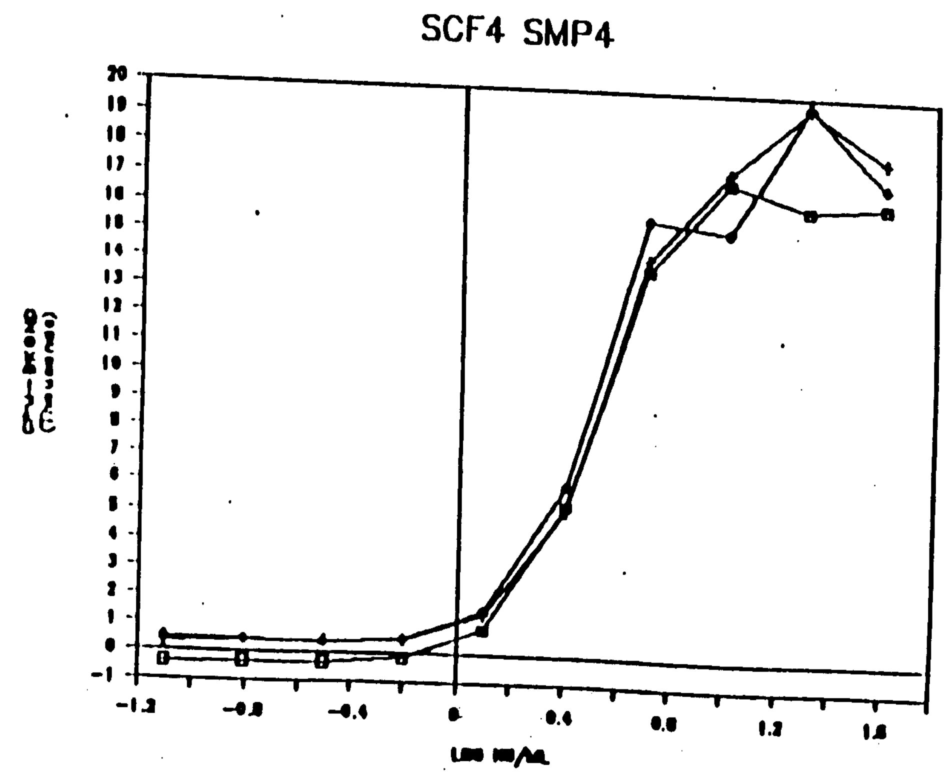

SCF4 SMP4
20
19
18
17
16
15
14
13
12
11
10
9
8
7
6
5
4
3
2
1
0
-1
-1.2
-0.8
-0.4
0
0.4
0.8
1.2
1.6

FIG. 32A

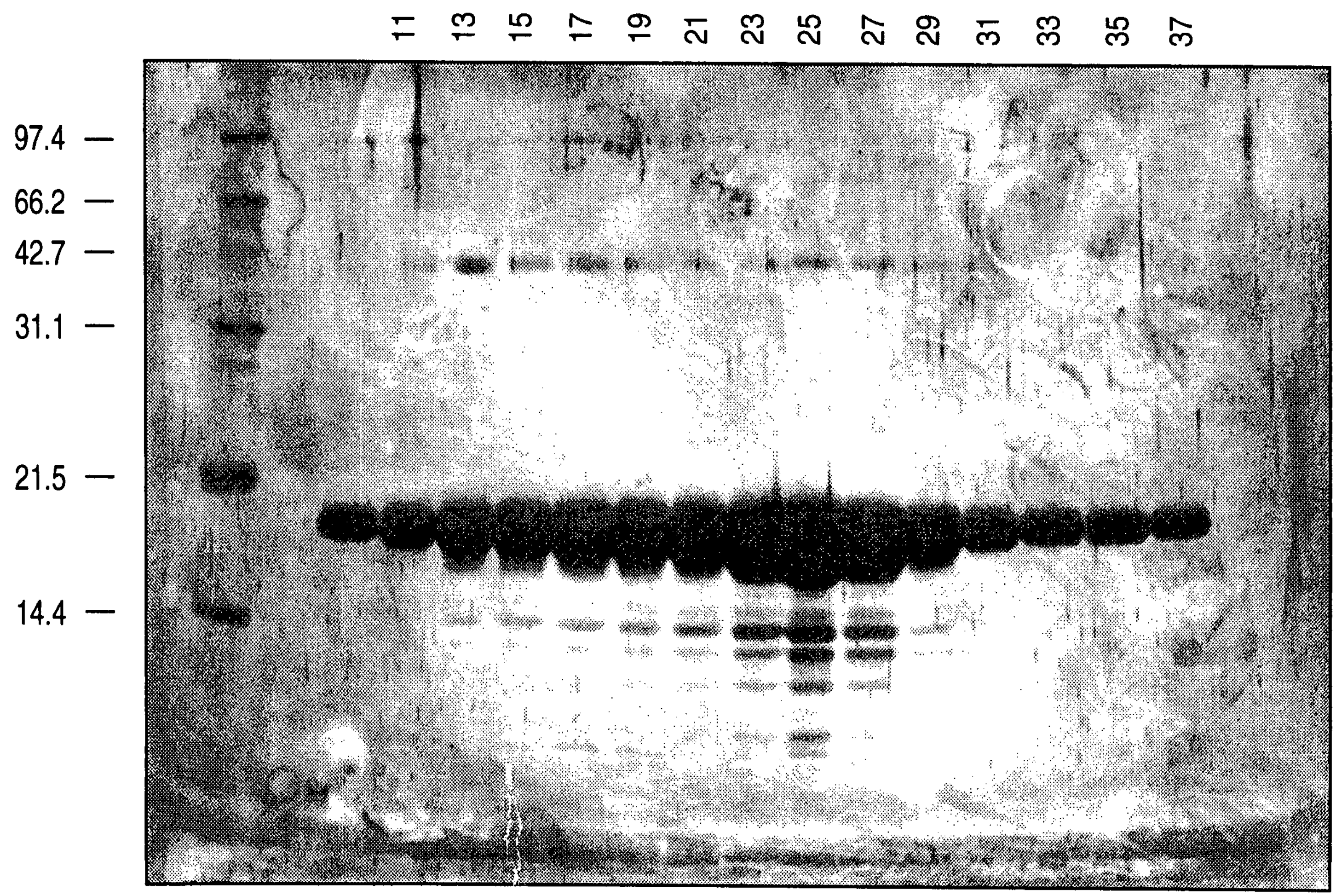


FIG. 32B

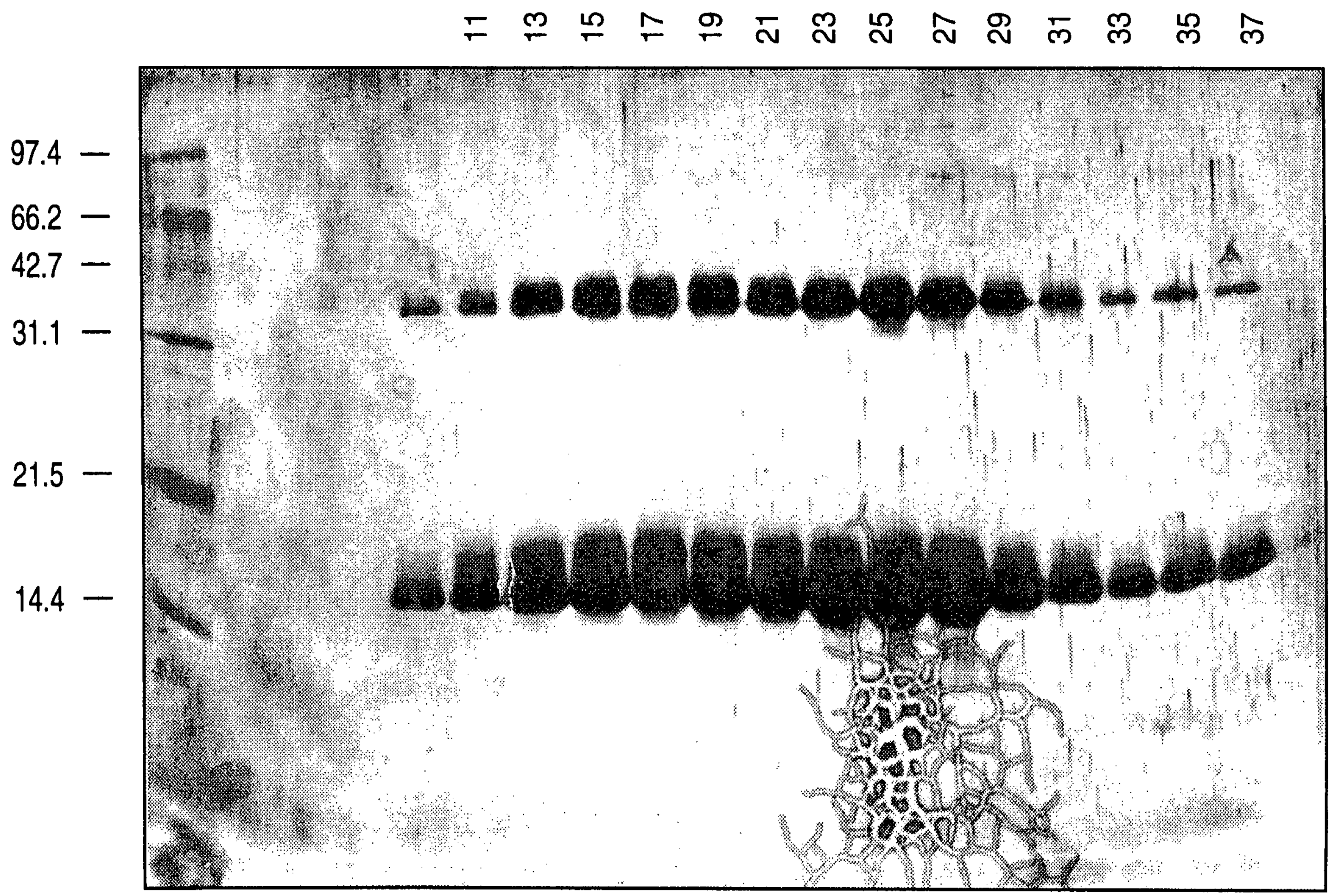
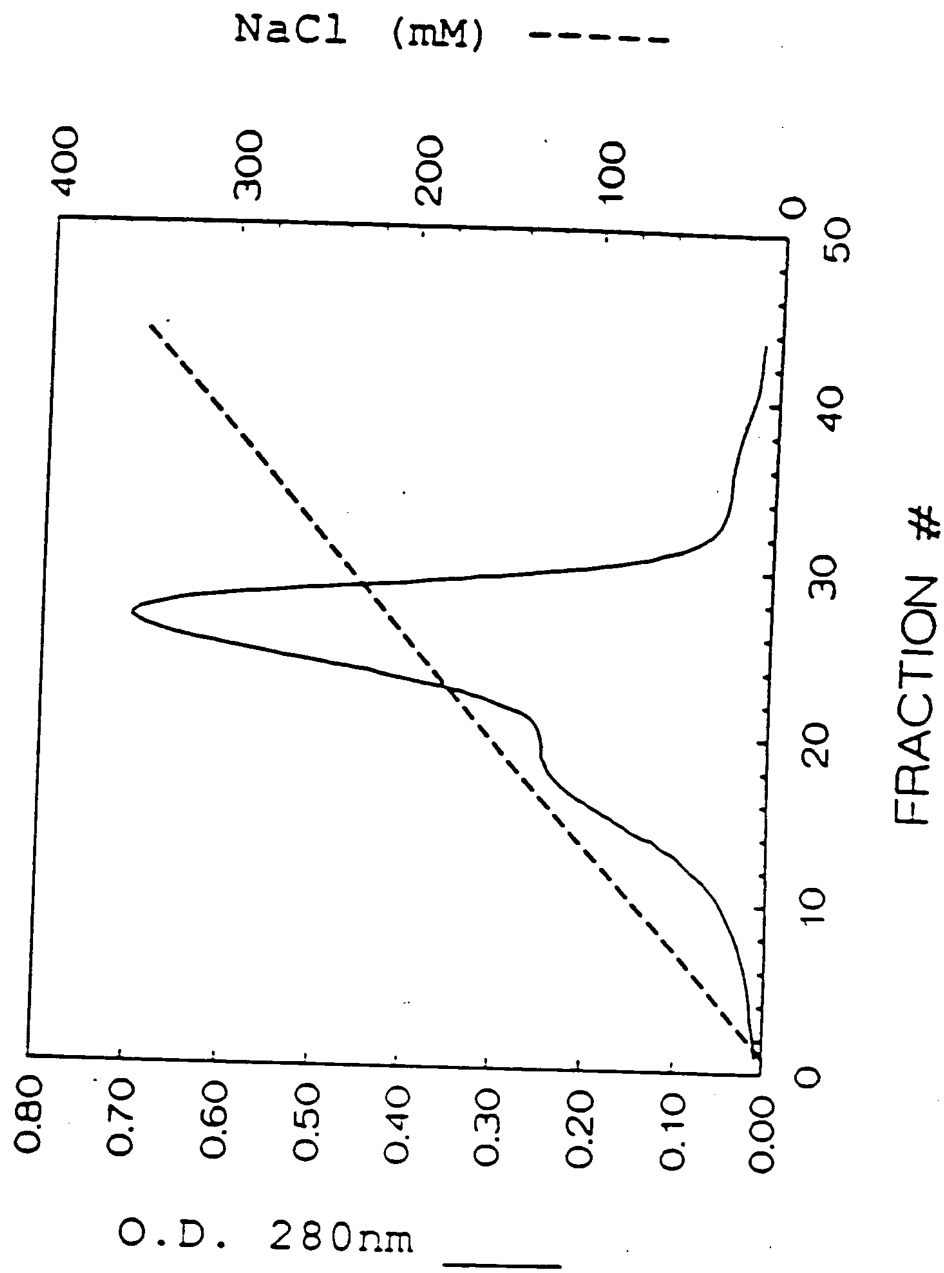


FIG.33



NaCl (mM) -----
400
300
200
100
0
0.80
0.70
0.60
0.50
0.40
0.30
0.20
0.10
0.00
0
10
20
30
40
50
FRACTION #
O.D. 280nm ____

FIG. 34A

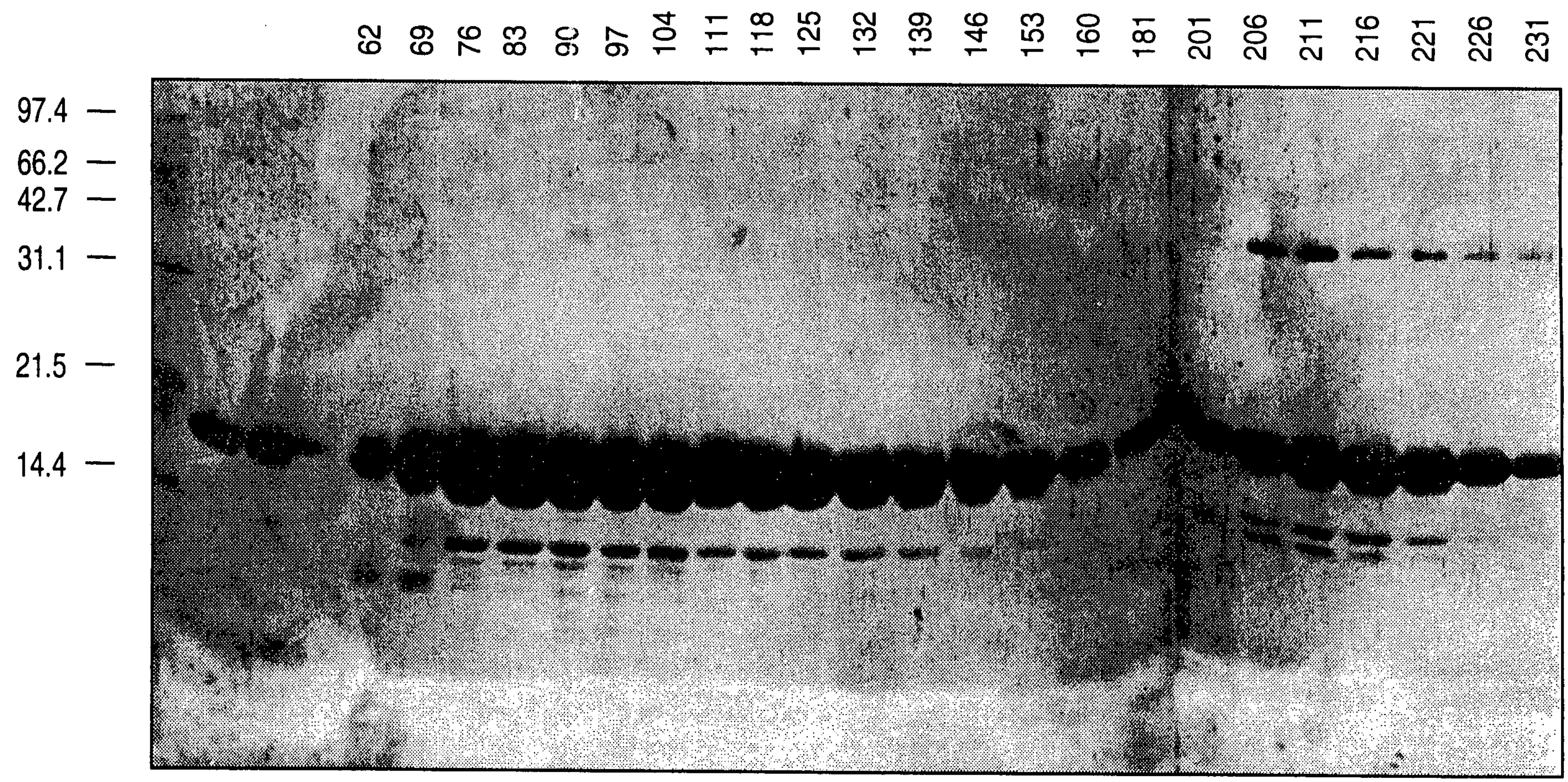
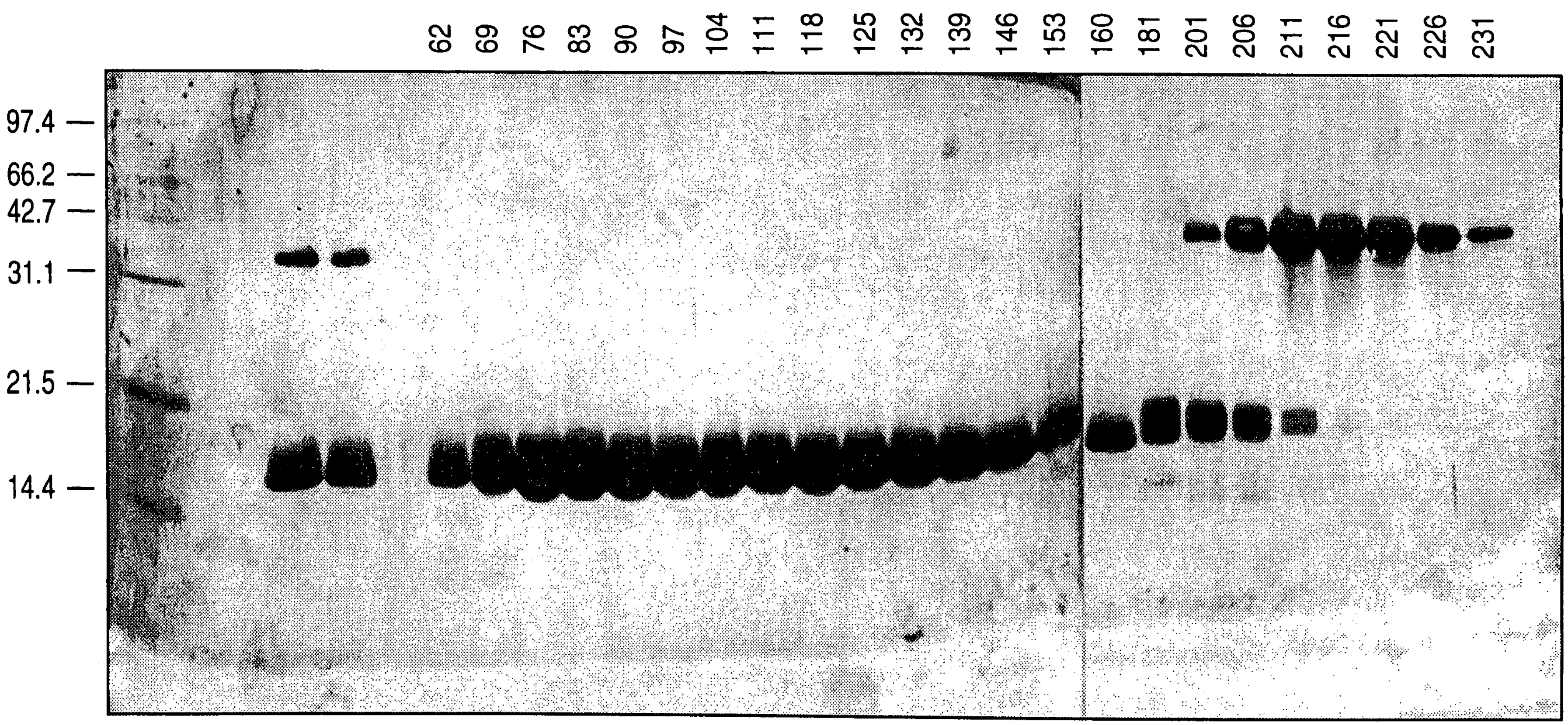

62
69
76
83
90
97
104
111
118
125
132
139
146
153
160
181
201
206
211
216
221
226
231
97.4
66.2
42.7
31.1
21.5
14.4

FIG. 34B



62
69
76
83
90
97
104
111
118
125
132
139
146
153
160
181
201
206
211
216
221
226
231
97.4
66.2
42.7
31.1
21.5
14.4

FIG. 35

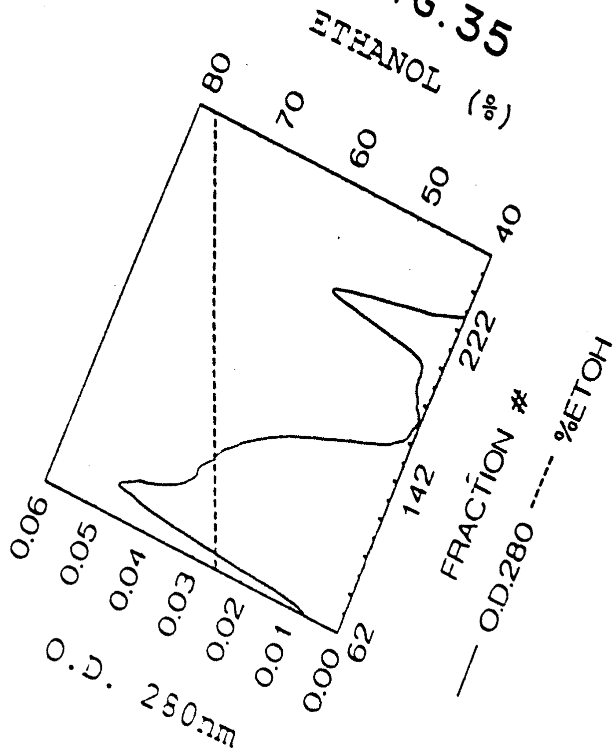
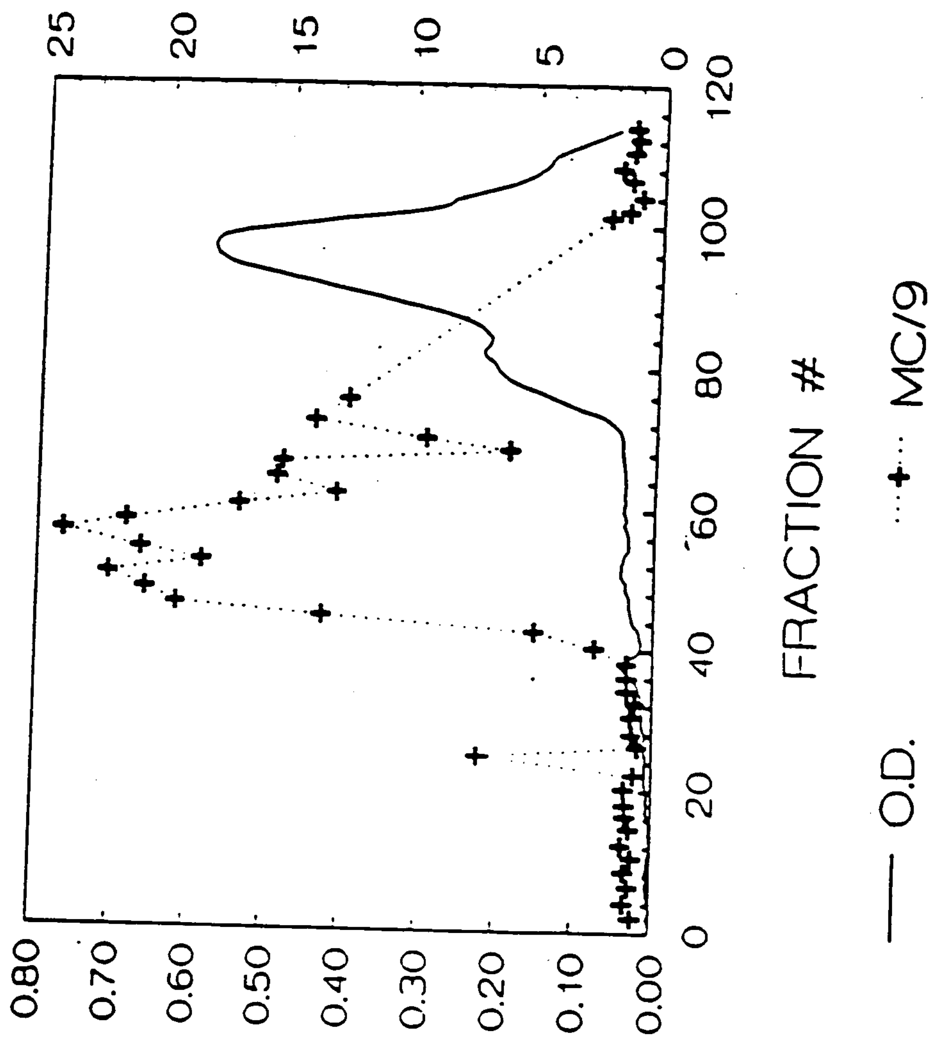

ETHANOL (%)
80
70
60
50
40
0.06
0.05
0.04
0.03
0.02
0.01
0.00
O.D. 280nm
62
142
222
FRACTION #
— O.D.280 ----- %ETOH

FIG. 36

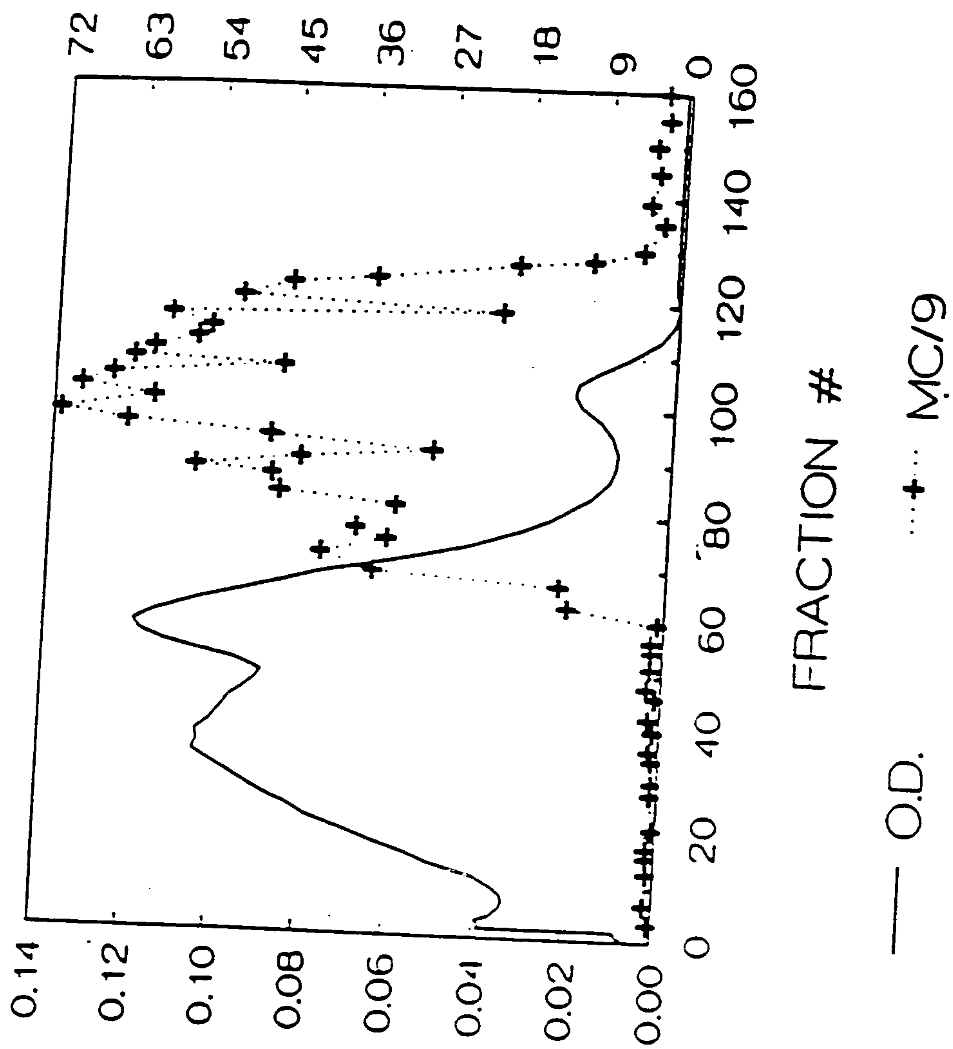
MC/9 CPM (x 10^{-3})



O.D. 280nm

FIG. 37

MC/9 CPM (x 10^{-3})



O.D. 280nm (x 10^{1})

FIG. 38

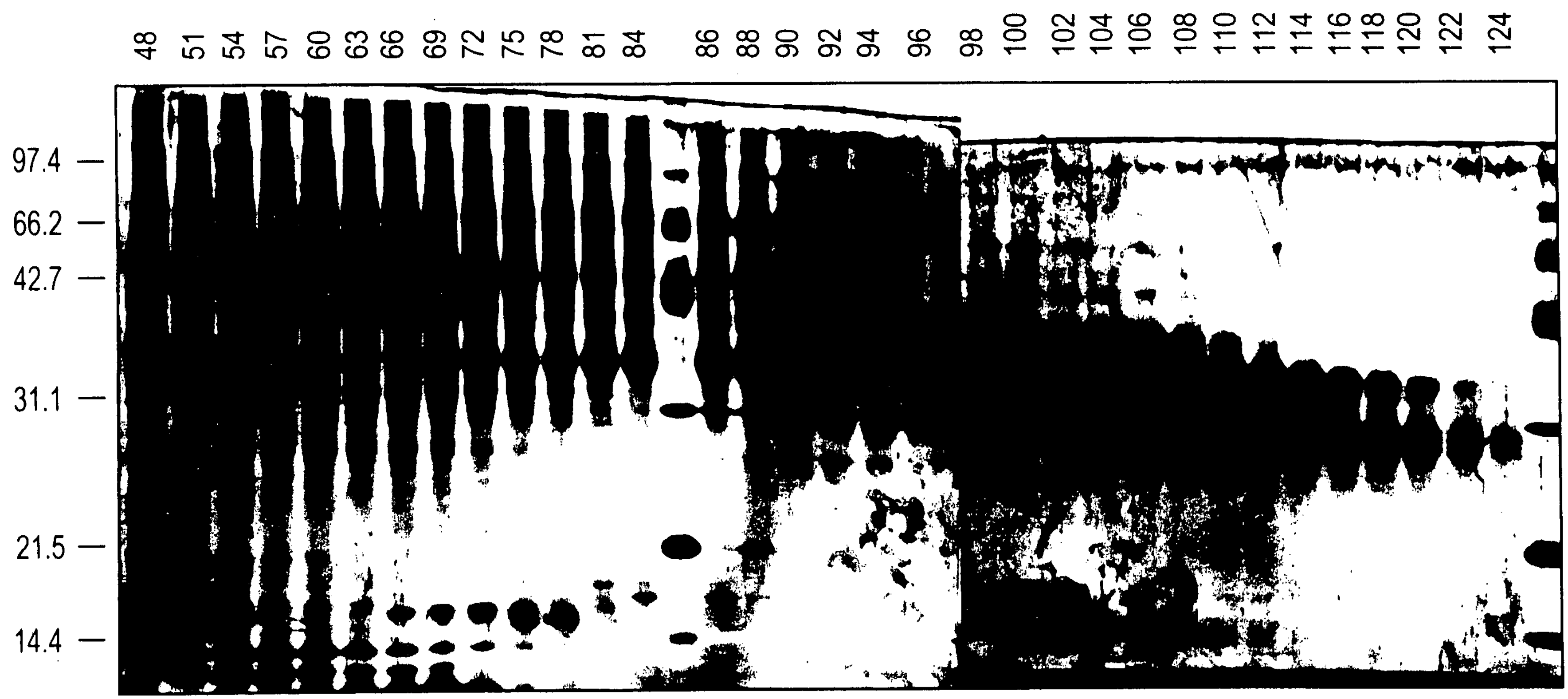

48
51
54
57
60
63
66
69
72
75
78
81
84
86
88
90
92
94
96
98
100
102
104
106
108
110
112
114
116
118
120
122
124
97.4
66.2
42.7
31.1
21.5
14.4

FIG. 39

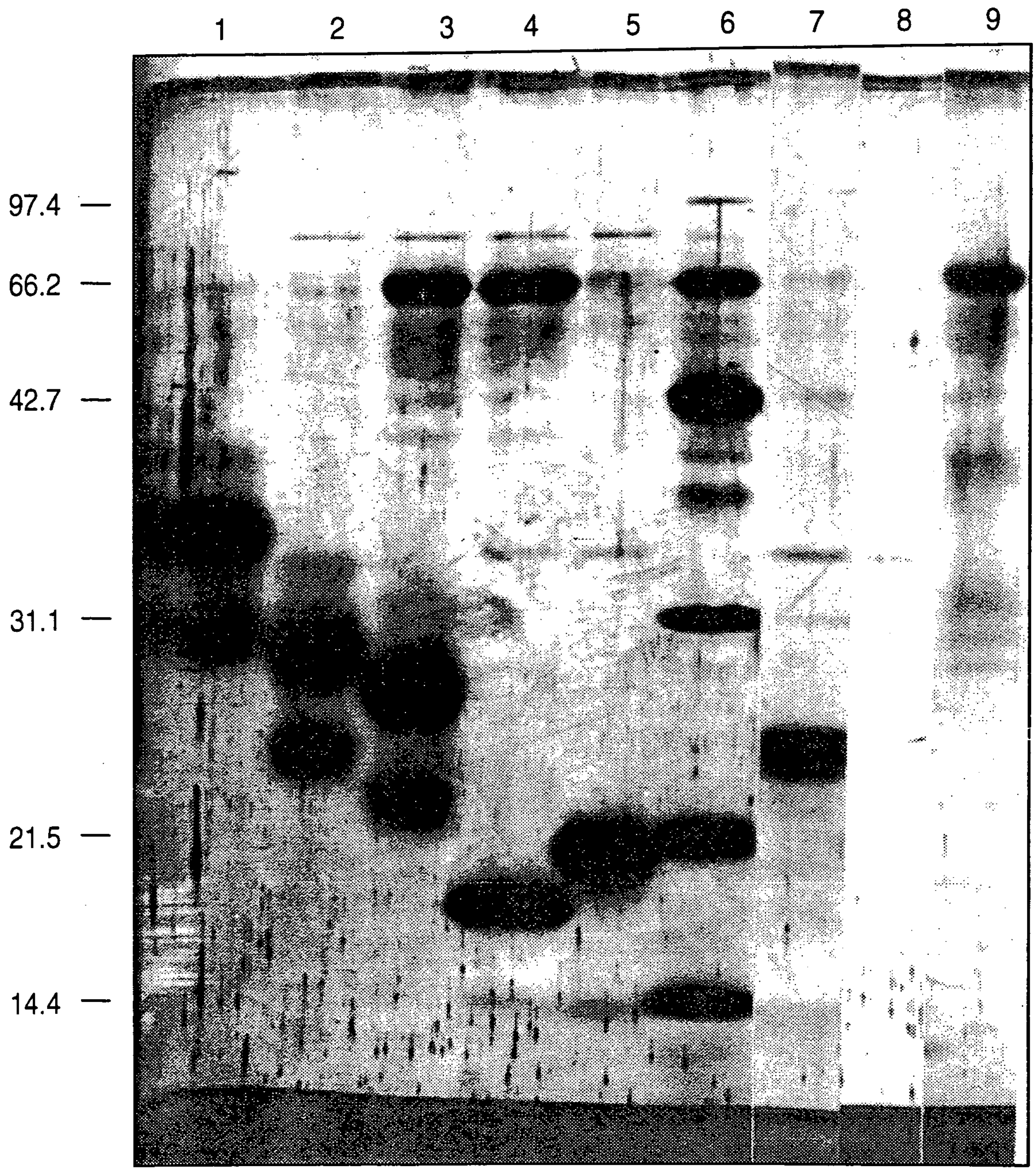


FIG. 40A

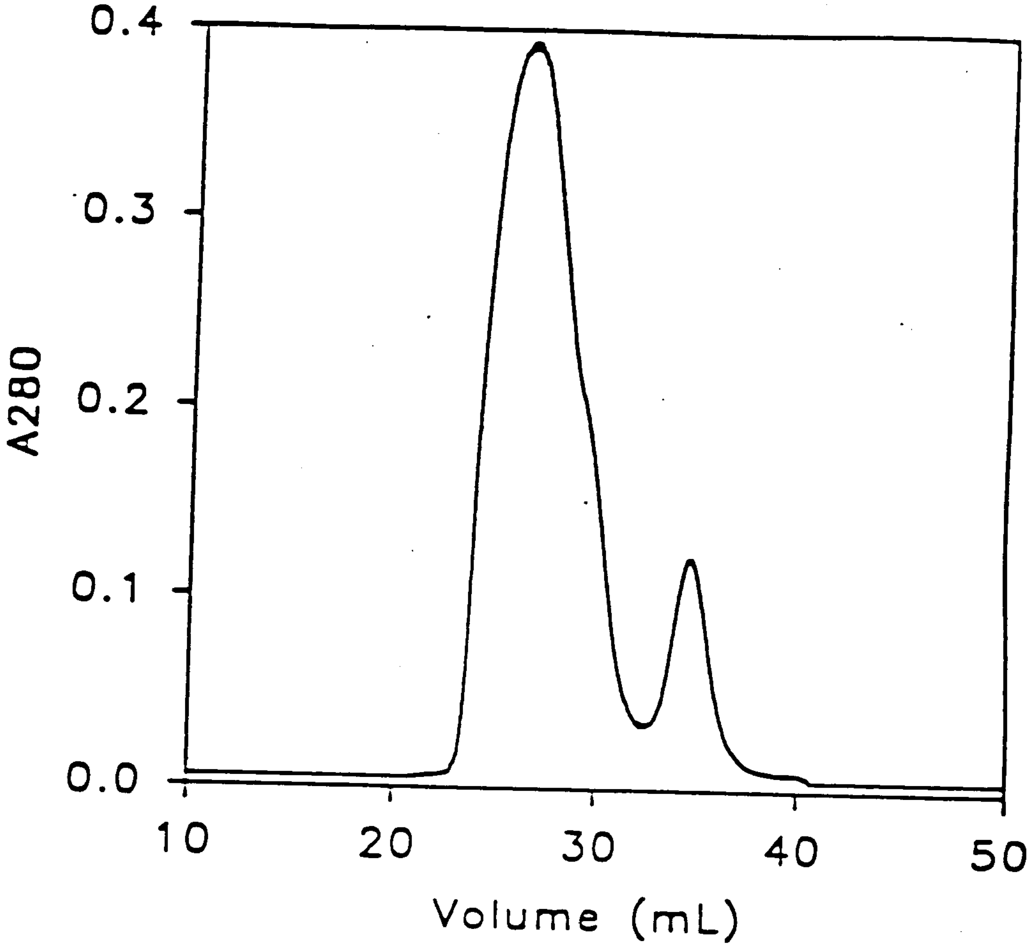


FIG. 40B

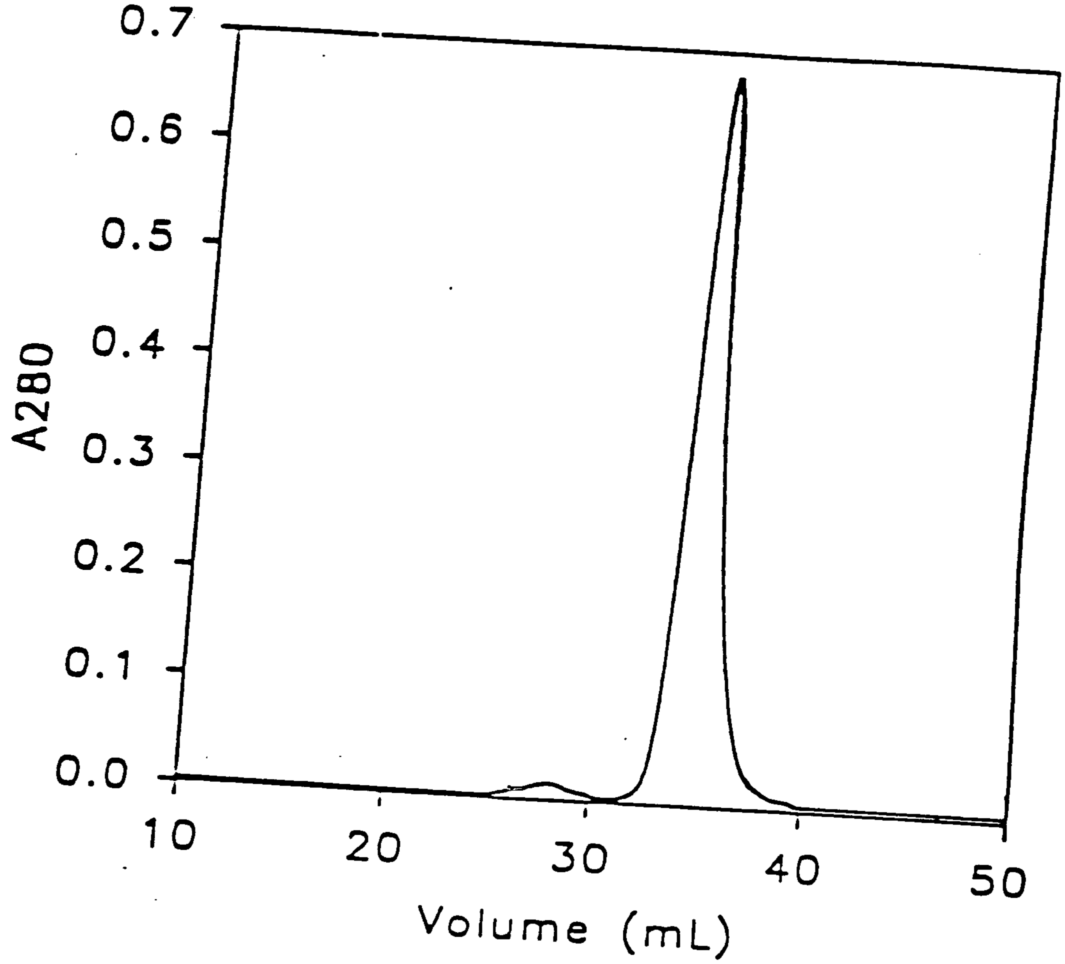


FIG. 41

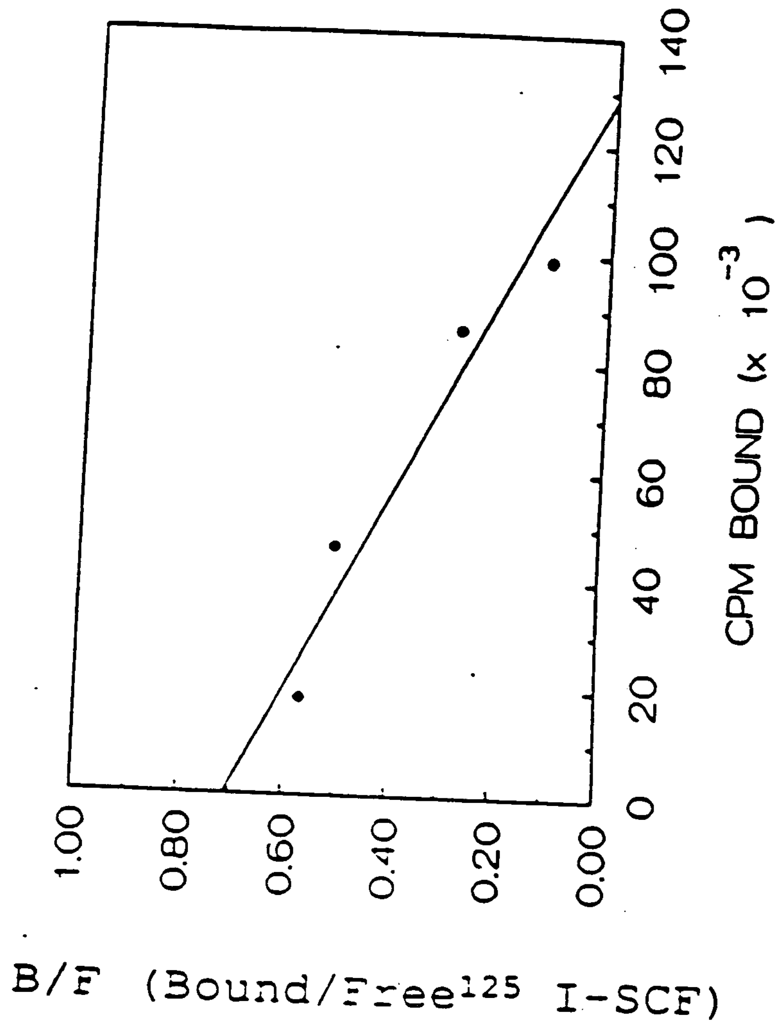

CPM BOUND (x 10^-3)
0
20
40
60
80
100
120
140
1.00
0.80
0.60
0.40
0.20
0.00
B/F (Bound/Free125 I-SCF)

FIG.42A

```
CCGCCTCGCGCCGAGACTAGAAGCGCTGCGGGAAGCAGGGACAGTGGAGAGGGCGCTGCGC  61

TCGGGCTACCCAATGCGTGGACTATCTGCCGCCGCTGTTCGTGCAATATGCTGGAGCTCCA 122

GAACAGCTAAACGGAGTCGCCACACCACTGTTTGTGCTGGATCGCAGCGCTGCCTTTCCTT 183

-25                 -20
Met Lys Lys Thr Gln Thr Trp Ile Leu Thr Cys Ile Tyr Leu Gln
ATG AAG AAG ACA CAA ACT TGG ATT CTC ACT TGC ATT TAT CTT CAG    228

-10                                      1
Leu Leu Leu Phe Asn Pro Leu Val Lys Thr Glu Gly Ile Cys Arg
CTG CTC CTA TTT AAT CCT CTC GTC AAA ACT GAA GGG ATC TGC AGG    273

                 10                                      20
Asn Arg Val Thr Asn Asn Val Lys Asp Val Thr Lys Leu Val Ala
AAT CGT GTG ACT AAT AAT GTA AAA GAC GTC ACT AAA TTG GTG GCA    318

                                     30
Asn Leu Pro Lys Asp Tyr Met Ile Thr Leu Lys Tyr Val Pro Gly
AAT CTT CCA AAA GAC TAC ATG ATA ACC CTC AAA TAT GTC CCC GGG    363

                 40                                      50
Met Asp Val Leu Pro Ser His Cys Trp Ile Ser Glu Met Val Val
ATG GAT GTT TTG CCA AGT CAT TGT TGG ATA AGC GAG ATG GTA GTA    408

                                     60
Gln Leu Ser Asp Ser Leu Thr Asp Leu Leu Asp Lys Phe Ser Asn
CAA TTG TCA GAC AGC TTG ACT GAT CTT CTG GAC AAG TTT TCA AAT    453
```

FIG. 42B

```
                        70                                                80
Ile Ser Glu Gly Leu Ser Asn Tyr Ser Ile Ile Asp Lys Leu Val
ATT TCT GAA GGC TTG AGT AAT TAT TCC ATC ATA GAC AAA CTT GTG   498

                                           90
Asn Ile Val Asp Asp Leu Val Glu Cys Val Lys Glu Asn Ser Ser
AAT ATA GTG GAT GAC CTT GTG GAG TGC GTG AAA GAA AAC TCA TCT   543

                   100                                    110
Lys Asp Leu Lys Lys Ser Phe Lys Ser Pro Glu Pro Arg Leu Phe
AAG GAT CTA AAA AAA TCA TTC AAG AGC CCA GAA CCC AGG CTC TTT   588

                                       120
Thr Pro Glu Glu Phe Phe Arg Ile Phe Asn Arg Ser Ile Asp Ala
ACT CCT GAA GAA TTC TTT AGA ATT TTT AAT AGA TCC ATT GAT GCC   633

                   130                                    140
Phe Lys Asp Phe Val Val Ala Ser Glu Thr Ser Asp Cys Val Val
TTC AAG GAC TTT GTA GTG GCA TCT GAA ACT AGT GAT TGT GTG GTT   678

                                       150
Ser Ser Thr Leu Ser Pro Glu Lys Asp Ser Arg Val Ser Val Thr
TCT TCA ACA TTA AGT CCT GAG AAA GAT TCC AGA GTC AGT GTC ACA   723
```

FIG.42C

```
                    160                                                  170
Lys Pro Phe Met Leu Pro Pro Val Ala Ala Ser Ser Leu Arg Asn
AAA CCA TTT ATG TTA CCC CCT GTT GCA GCC AGC TCC CTT AGG AAT    768

                                          180
Asp Ser Ser Ser Ser Asn Arg Lys Ala Lys Asn Pro Pro Gly Asp
GAC AGC AGT AGC AGT AAT AGG AAG GCC AAA AAT CCC CCT GGA GAC    813

                    190                                      200
Ser Ser Leu His Trp Ala Ala Met Ala Leu Pro Ala Leu Phe Ser
TCC AGC CTA CAC TGG GCA GCC ATG GCA TTG CCA GCA TTG TTT TCT    858

                                          210
Leu Ile Ile Gly Phe Ala Phe Gly Ala Leu Tyr Trp Lys Lys Arg
CTT ATA ATT GGC TTT GCT TTT GGA GCC TTA TAC TGG AAG AAG AGA    903

                    220                                      230
Gln Pro Ser Leu Thr Arg Ala Val Glu Asn Ile Gln Ile Asn Glu
CAG CCA AGT CTT ACA AGG GCA GTT GAA AAT ATA CAA ATT AAT GAA    948

                                      240
Glu Asp Asn Glu Ile Ser Met Leu Gln Glu Lys Glu Arg Glu Phe
GAG GAT AAT GAG ATA AGT ATG TTG CAA GAG AAA GAG AGA GAG TTT    993

        248
Gln Glu Val End
CAA GAA GTG TAA    TTGTGGCTTGTATCAACACTGTTACTTTCGTACATTGGC 1044
```

FIG. 42D

TGGTAACAGTTCATGTTTGCTTCATAAATGAAGCAGCTTTAAACAAATTCATATTCTGTC 1104

TGGAGTGACAGACCACATCTTTATCTGTTCTTGCTACCCATGACTTTATATGGATGATTC 1164

AGAAATTGGAACAGAATGTTTTACTGTGAAACTGGCACTGAATTAATCATCTATAAAGAA 1224

GAACTTGCATGGAGCAGGACTCTATTTTAAGGACTGCGGGACTTGGGTCTCATTTAGAAC 1284

TTGCAGCTGATGTTGGAAGAGAAAGCACGTGTCTCAGACTGCATGTACCATTTGCATGGC 1344

TCCAGAAATGTCTAAATGCTGAAAAAACACCTAGCTTTATTCTTCAGATACAAACTGCAG 1404

FIG. 43

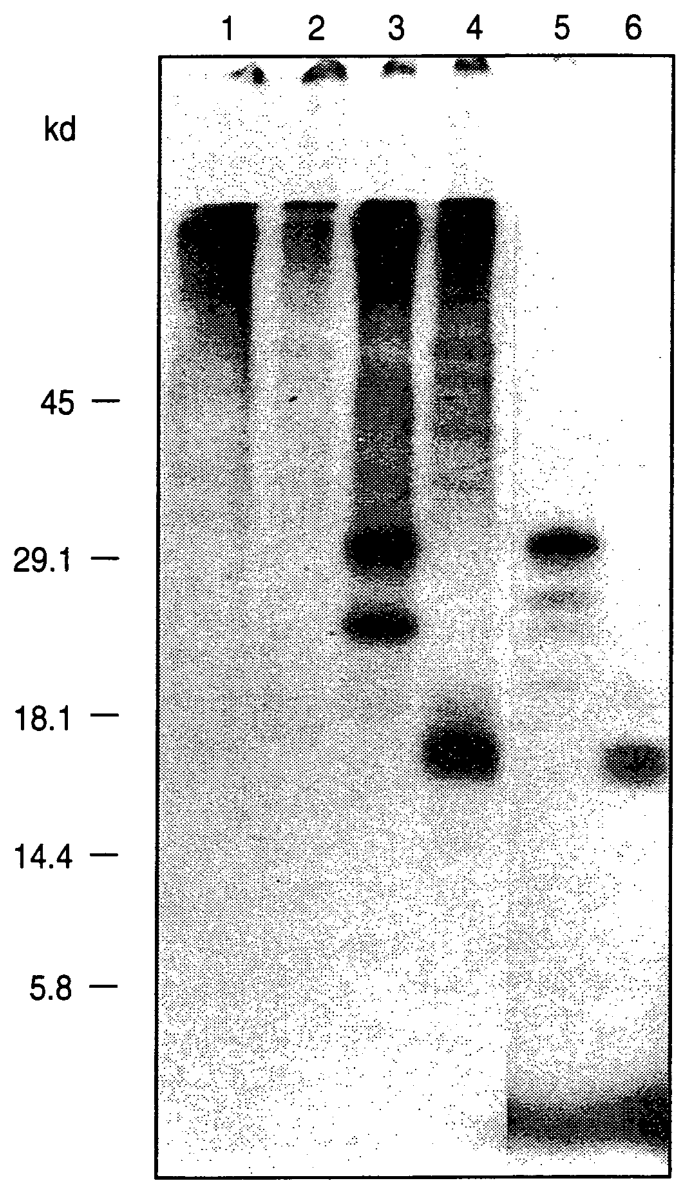


FIG. 44A

```
                                      AGCAGGGACAGTGGAGAGGGCGCTGCGCTC    30

GGGCTACCCAATGCGTGGACTATCTGCCGCCGCTGTTCGTGCAATATGCTGGAGCTCCAG    90

AACAGCTAAACGGAGTCGCCACACCACTGTTTGTGCTGGATCGCAGCGCTGCCTTTCCTT   150

-25                 -20
Met Lys Lys Thr Gln Thr Trp Ile Leu Thr Cys Ile Tyr Leu Gln
ATG AAG AAG ACA CAA ACT TGG ATT CTC ACT TGC ATT TAT CTT CAG    195

-10                                     1
Leu Leu Leu Phe Asn Pro Leu Val Lys Thr Glu Gly Ile Cys Arg
CTG CTC CTA TTT AAT CCT CTC GTC AAA ACT GAA GGG ATC TGC AGG    240

                 10                                      20
Asn Arg Val Thr Asn Asn Val Lys Asp Val Thr Lys Leu Val Ala
AAT CGT GTG ACT AAT AAT GTA AAA GAC GTC ACT AAA TTG GTG GCA    285

                                    30
Asn Leu Pro Lys Asp Tyr Met Ile Thr Leu Lys Tyr Val Pro Gly
AAT CTT CCA AAA GAC TAC ATG ATA ACC CTC AAA TAT GTC CCC GGG    330

                 40                                      50
Met Asp Val Leu Pro Ser His Cys Trp Ile Ser Glu Met Val Val
ATG GAT GTT TTG CCA AGT CAT TGT TGG ATA AGC GAG ATG GTA GTA    375
```

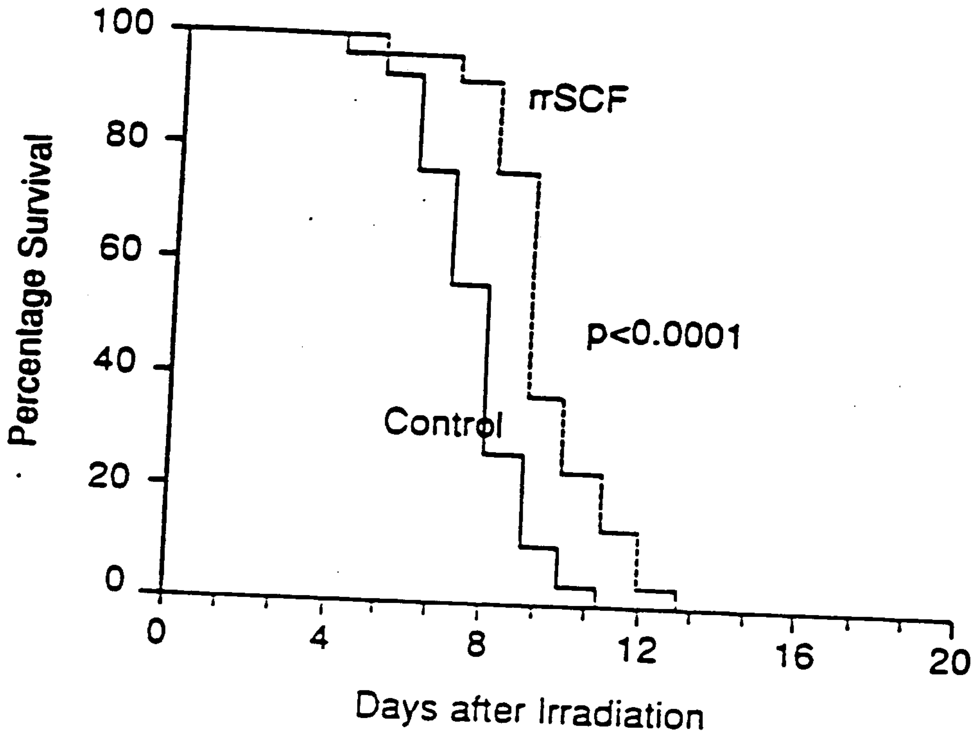
FIG. 44B

```
                                                60
Gln Leu Ser Asp Ser Leu Thr Asp Leu Leu Asp Lys Phe Ser Asn
CAA TTG TCA GAC AGC TTG ACT GAT CTT CTG GAC AAG TTT TCA AAT   420

                 70                                     80
Ile Ser Glu Gly Leu Ser Asn Tyr Ser Ile Ile Asp Lys Leu Val
ATT TCT GAA GGC TTG AGT AAT TAT TCC ATC ATA GAC AAA CTT GTG   465

                                         90
Asn Ile Val Asp Asp Leu Val Glu Cys Val Lys Glu Asn Ser Ser
AAT ATA GTG GAT GAC CTT GTG GAG TGC GTG AAA GAA AAC TCA TCT   510

                100                                    110
Lys Asp Leu Lys Lys Ser Phe Lys Ser Pro Glu Pro Arg Leu Phe
AAG GAT CTA AAA AAA TCA TTC AAG AGC CCA GAA CCC AGG CTC TTT   555

                                        120
Thr Pro Glu Glu Phe Phe Arg Ile Phe Asn Arg Ser Ile Asp Ala
ACT CCT GAA GAA TTC TTT AGA ATT TTT AAT AGA TCC ATT GAT GCC   600

                130                                    140
Phe Lys Asp Phe Val Val Ala Ser Glu Thr Ser Asp Cys Val Val
TTC AAG GAC TTT GTA GTG GCA TCT GAA ACT AGT GAT TGT GTG GTT   645

                                        150
Ser Ser Thr Leu Ser Pro Glu Lys|Gly|Lys Ala Lys Asn Pro Pro
TCT TCA ACA TTA AGT CCT GAG AAA|GGG|AAG GCC AAA AAT CCC CCT   690
```

FIG.44C

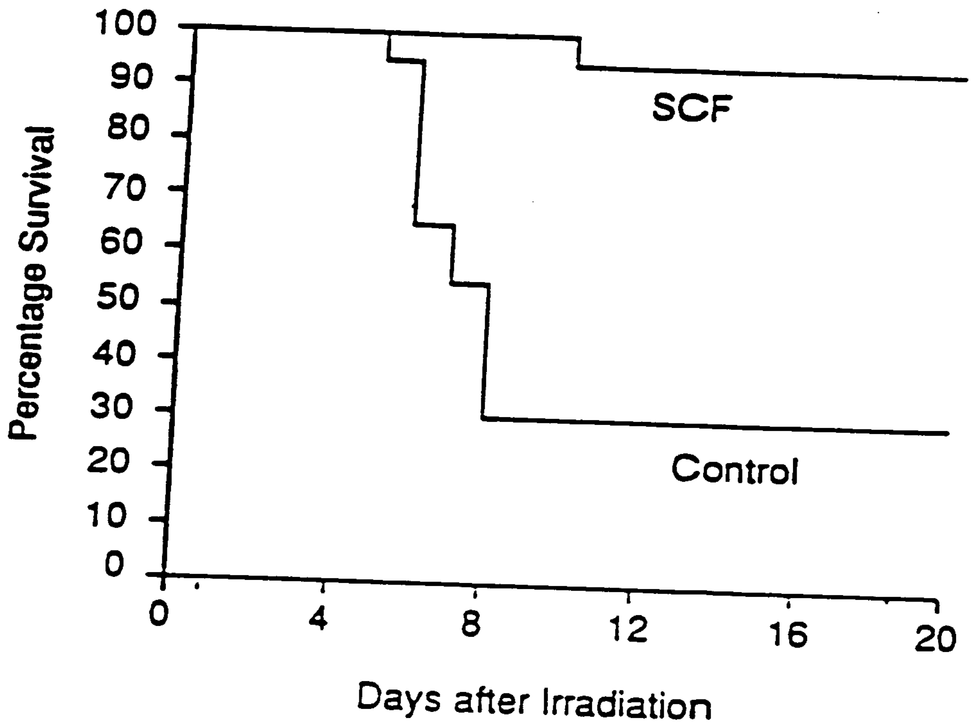
```
                    160                                                170
Gly Asp Ser Ser Leu His Trp Ala Ala Met Ala Leu Pro Ala Leu
GGA GAC TCC AGC CTA CAC TGG GCA GCC ATG GCA TTG CCA GCA TTG    735

                                        180
Phe Ser Leu Ile Ile Gly Phe Ala Phe Gly Ala Leu Tyr Trp Lys
TTT TCT CTT ATA ATT GGC TTT GCT TTT GGA GCC TTA TAC TGG AAG    780

                    190                                    200
Lys Arg Gln Pro Ser Leu Thr Arg Ala Val Glu Asn Ile Gln Ile
AAG AGA CAG CCA AGT CTT ACA AGG GCA GTT GAA AAT ATA CAA ATT    825

                                        210
Asn Glu Glu Asp Asn Glu Ile Ser Met Leu Gln Glu Lys Glu Arg
AAT GAA GAG GAT AAT GAG ATA AGT ATG TTG CAA GAG AAA GAG AGA    870

                    220
Glu Phe Gln Glu Val End
GAG TTT CAA GAA GTG TAA     TTGTGGCTTGTATCAACACTGTTACTTTCGTA    920

CATTGGCTGGTAACAGTTCATGTTTGCTTCATAAATGAAGCAGCTTTAAACAAATTCATA    980

TTCTGTCTGGAGTGACAGACCACATCTTTATCTGTTCTTGCTACCCATGACTTTATATGG   1040

ATGATTCAGAAATTGGAACAGAATGTTTTACTGTGAAACTGGCACTGA               1088
```

FIG.45



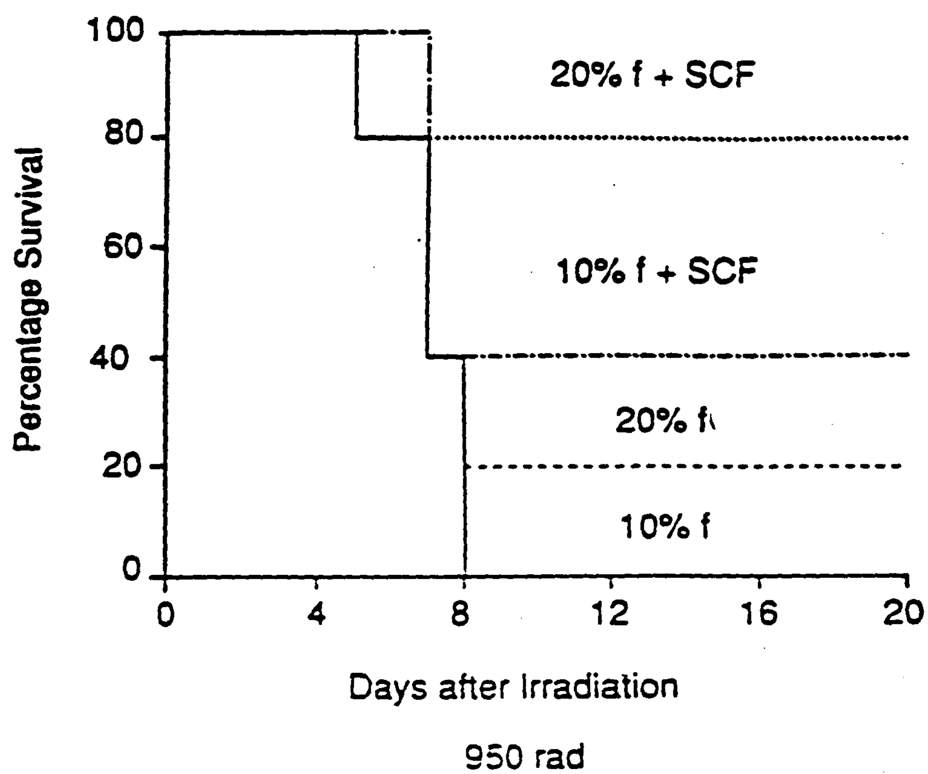
rrSCF
p<0.0001
Control
Percentage Survival
100
80
60
40
20
0
0
4
8
12
16
20
Days after Irradiation

FIG. 46



850 RADS; 5% of femur transplanted

FIG. 47



100
80
60
40
20
0
Percentage Survival
20% f + SCF
10% f + SCF
20% f
10% f
0
4
8
12
16
20
Days after Irradiation
950 rad

FIG. 48

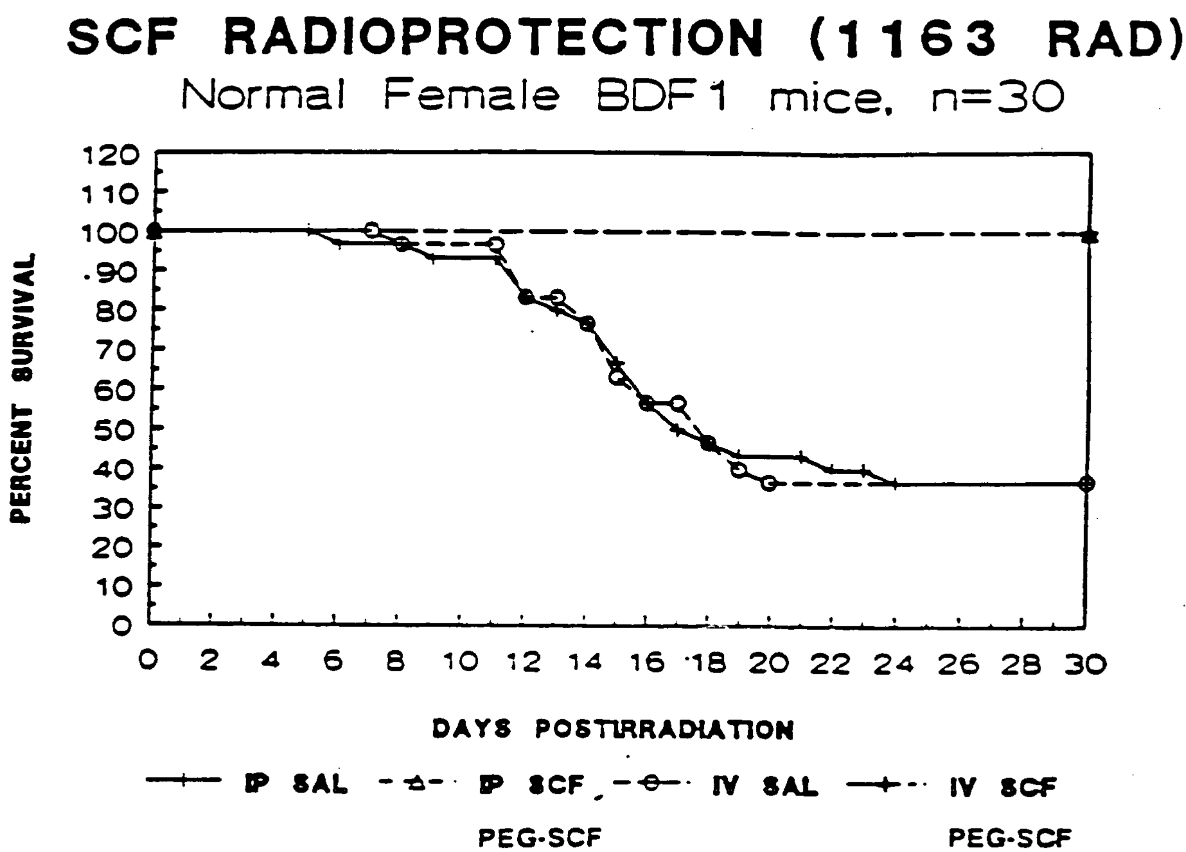
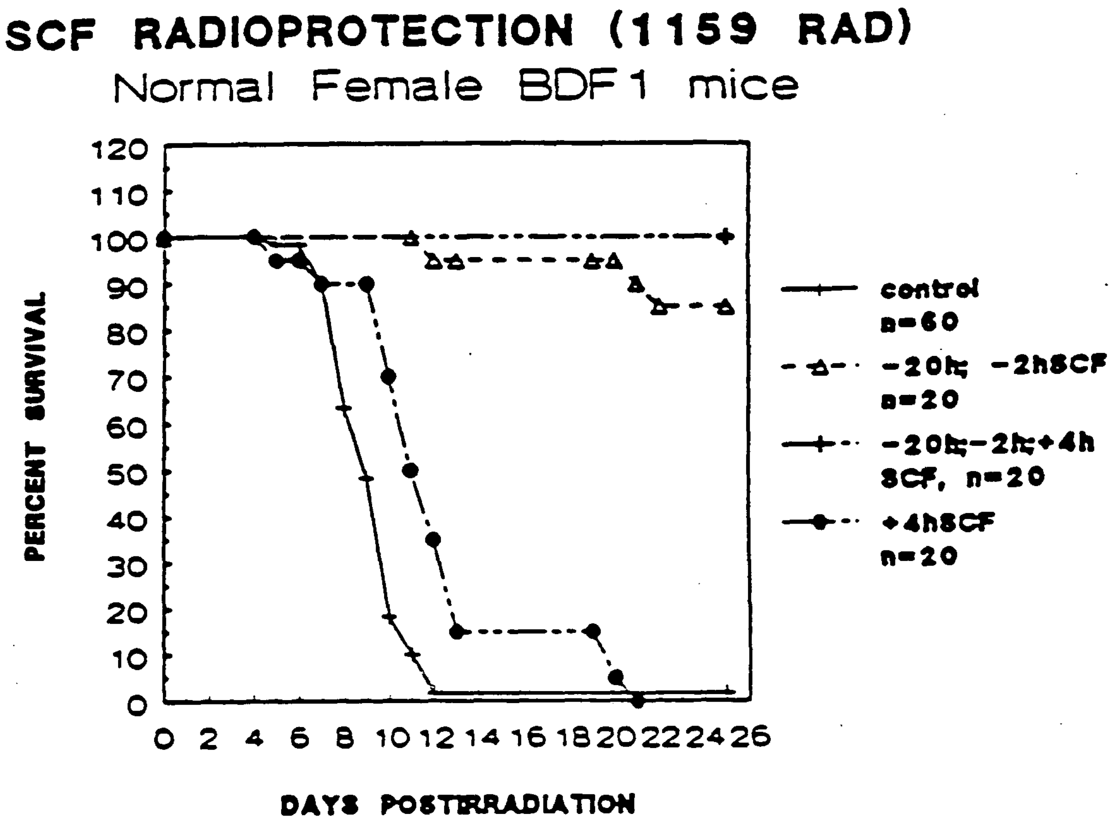
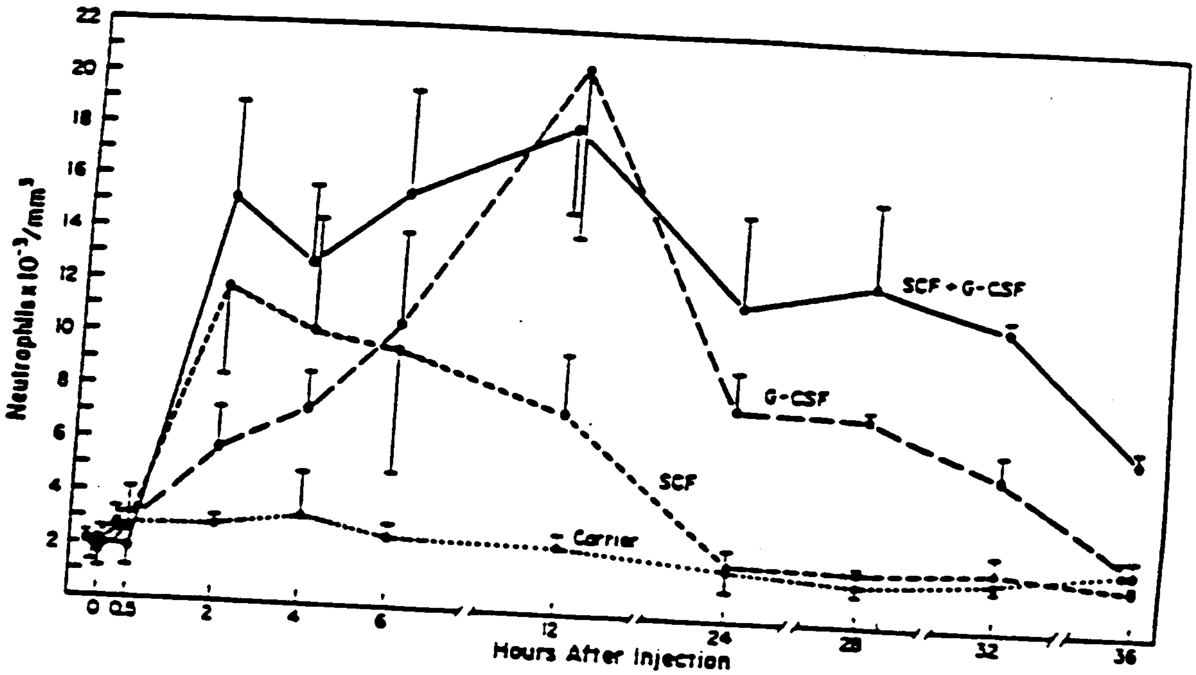

SCF RADIOPROTECTION (1163 RAD)
Normal Female BDF1 mice, n=30
PERCENT SURVIVAL
120
110
100
90
80
70
60
50
40
30
20
10
0
0 2 4 6 8 10 12 14 16 18 20 22 24 26 28 30
DAYS POSTIRRADIATION
IP SAL
IP SCF PEG-SCF
IV SAL
IV SCF PEG-SCF

FIG. 49



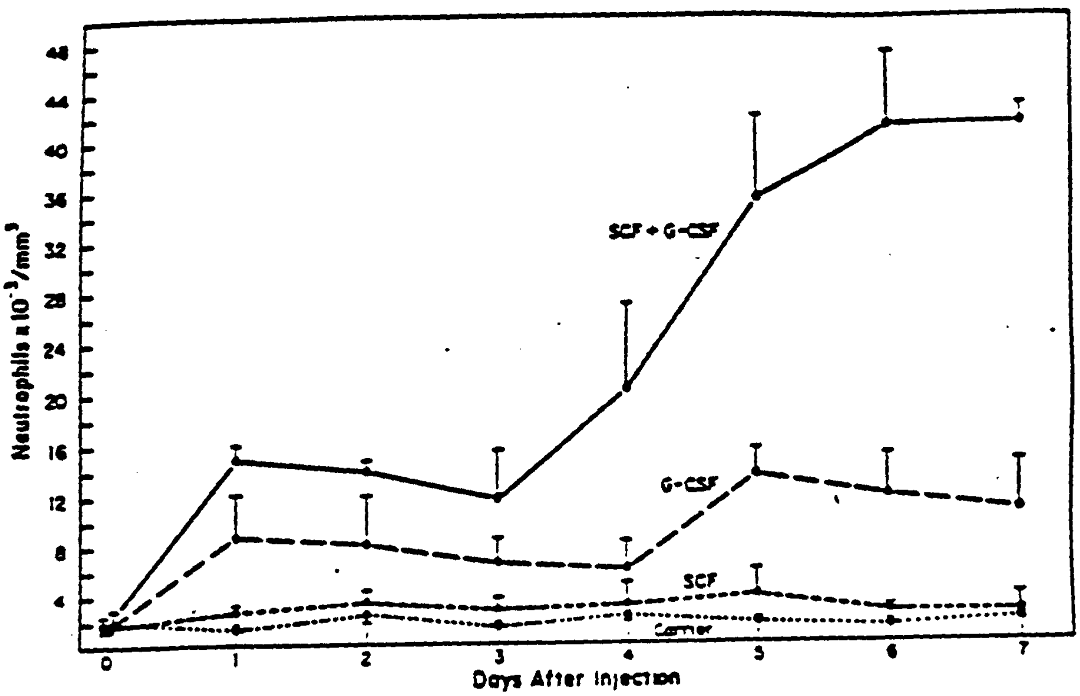
SCF RADIOPROTECTION (1159 RAD)
Normal Female BDF1 mice
PERCENT SURVIVAL
120
110
100
90
80
70
60
50
40
30
20
10
0
0 2 4 6 8 10 12 14 16 18 20 22 24 26
DAYS POSTIRRADIATION
control
n=60
-20h; -2hSCF
n=20
-20h;-2h;+4h
SCF, n=20
+4hSCF
n=20

FIG. 50



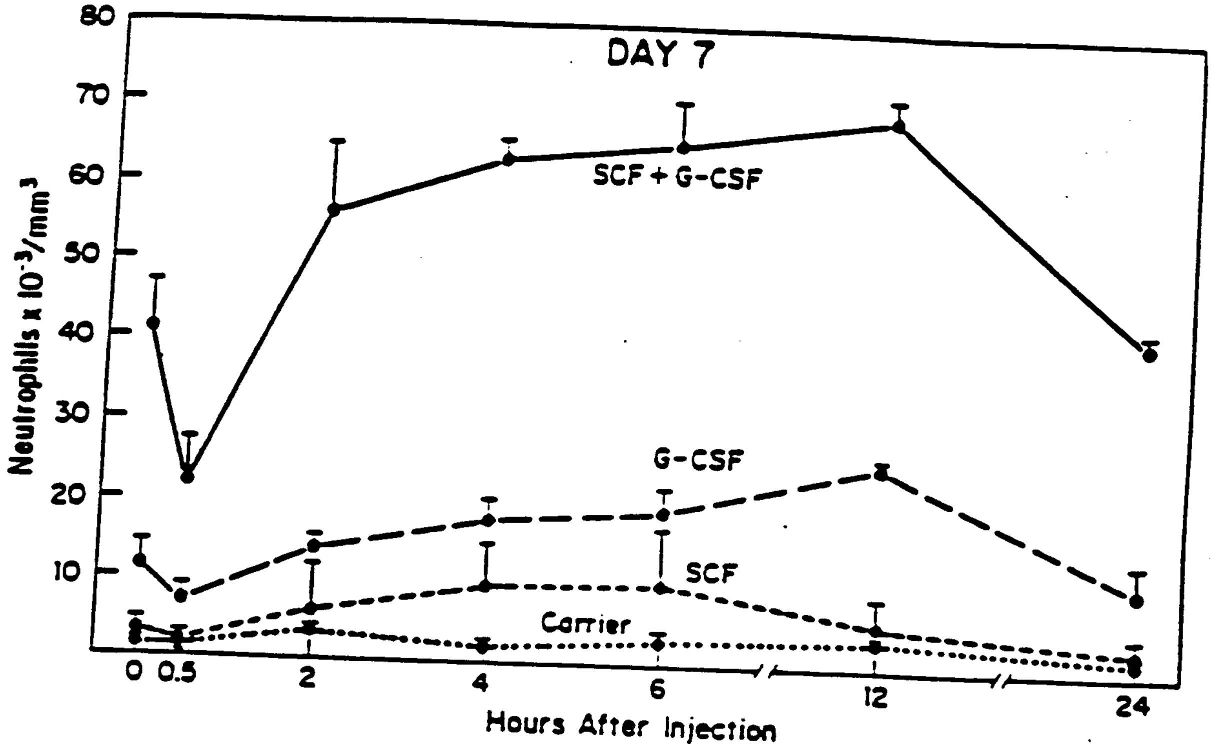
Neutrophils x 10^-3/mm^3
22
20
18
16
14
12
10
8
6
4
2
0
0.5
2
4
6
12
24
28
32
36
Hours After Injection
SCF + G-CSF
G-CSF
SCF
Carrier

FIG. 51



Neutrophils x 10^{-3}/mm^3
48
44
40
36
32
28
24
20
16
12
8
4
SCF + G-CSF
G-CSF
SCF
Carrier
0
1
2
3
4
5
6
7
Days After Injection

FIG. 52



DAY 7
SCF + G-CSF
G-CSF
SCF
Carrier
Neutrophils x 10^{-3}/mm^3
80
70
60
50
40
30
20
10
0
0.5
2
4
6
12
24
Hours After Injection

FIG. 53

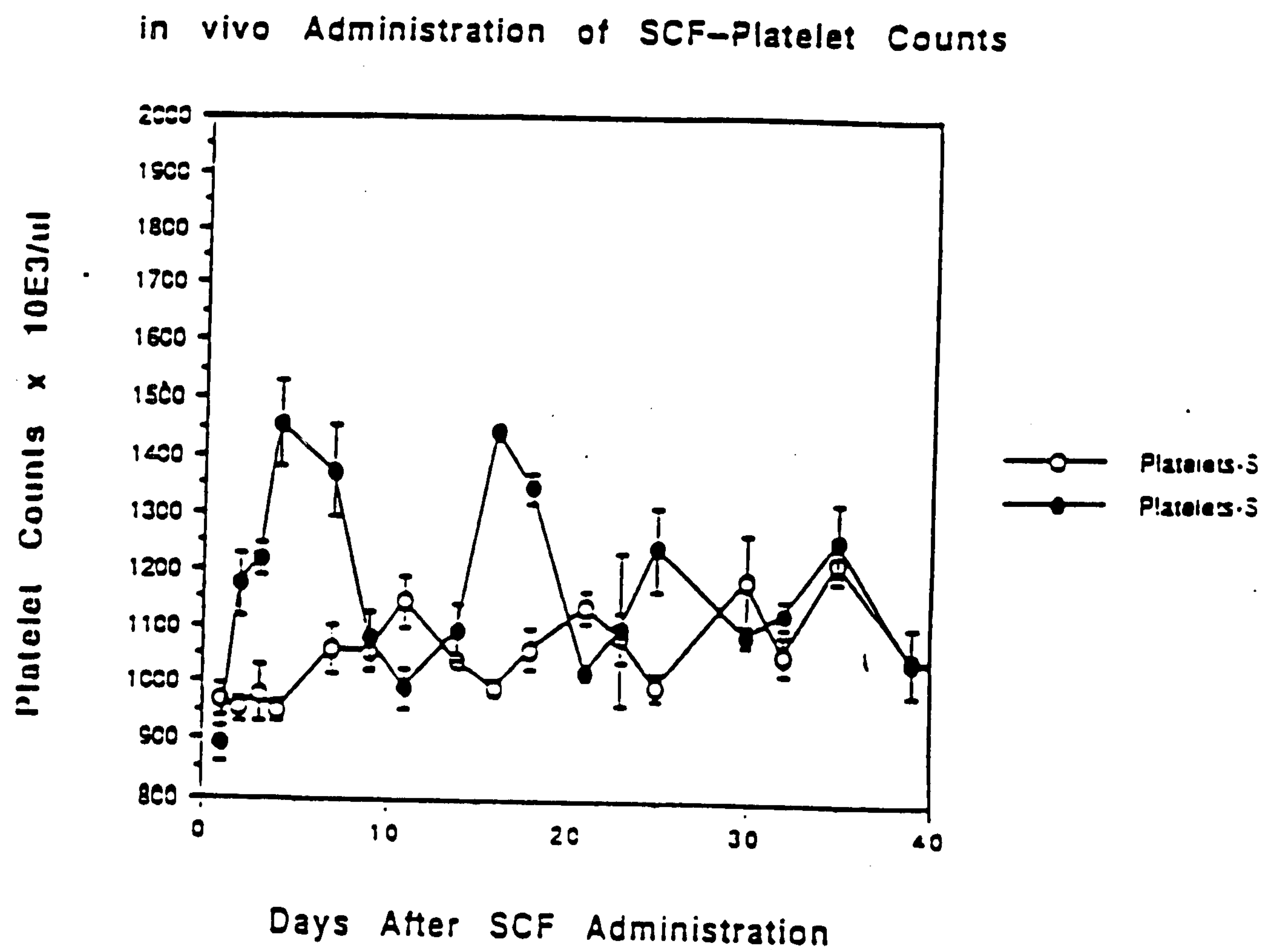

in vivo Administration of SCF–Platelet Counts
Platelet Counts x 10E3/ul
2000
1900
1800
1700
1600
1500
1400
1300
1200
1100
1000
900
800
0
10
20
30
40
Days After SCF Administration
Platelets-S
Platelets-S

FIG. 54

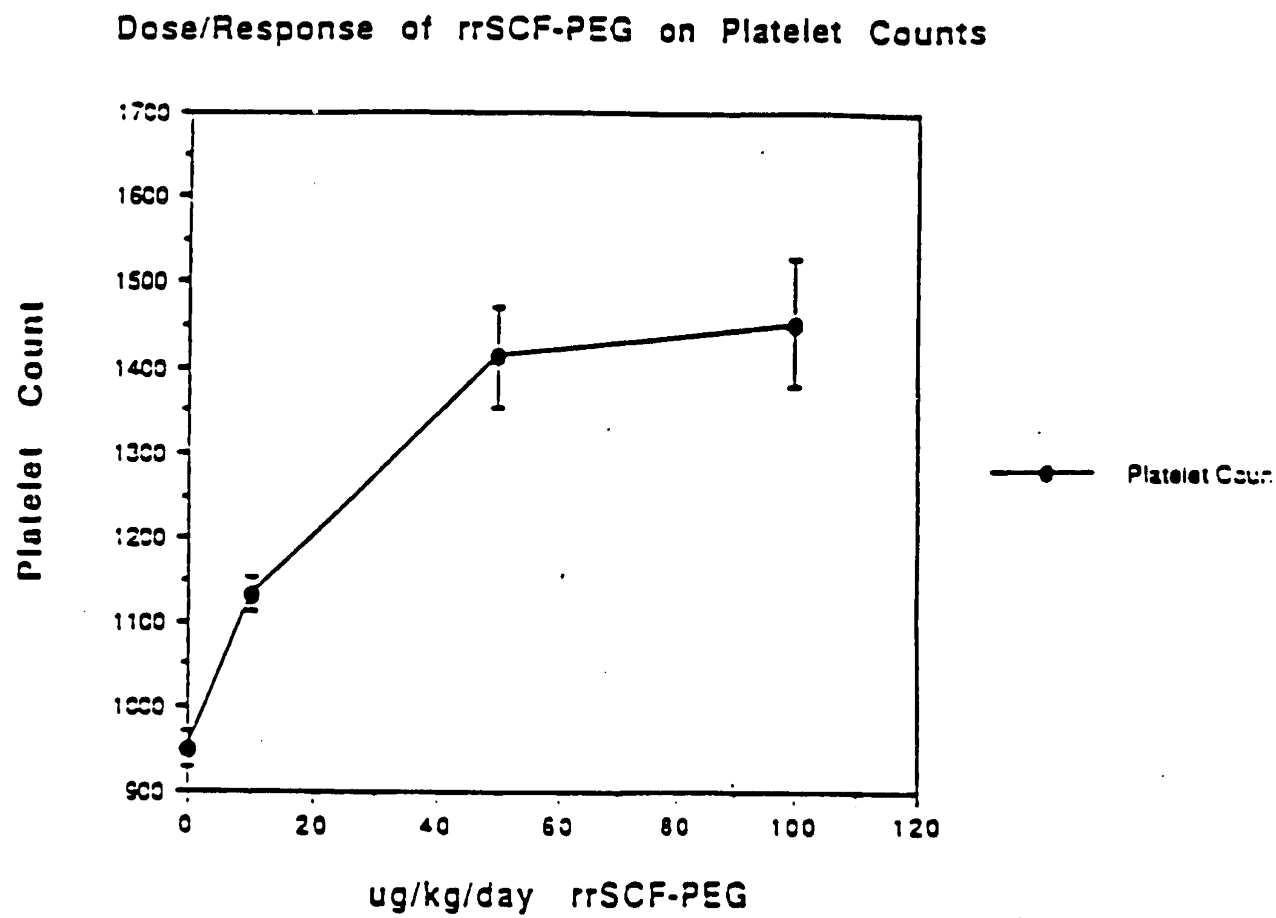

Dose/Response of rrSCF-PEG on Platelet Counts
Platelet Count
1700
1600
1500
1400
1300
1200
1100
1000
900
0
20
40
60
80
100
120
ug/kg/day rrSCF-PEG
Platelet Count

FIG. 55

Effect of 5-FU on platelet levels

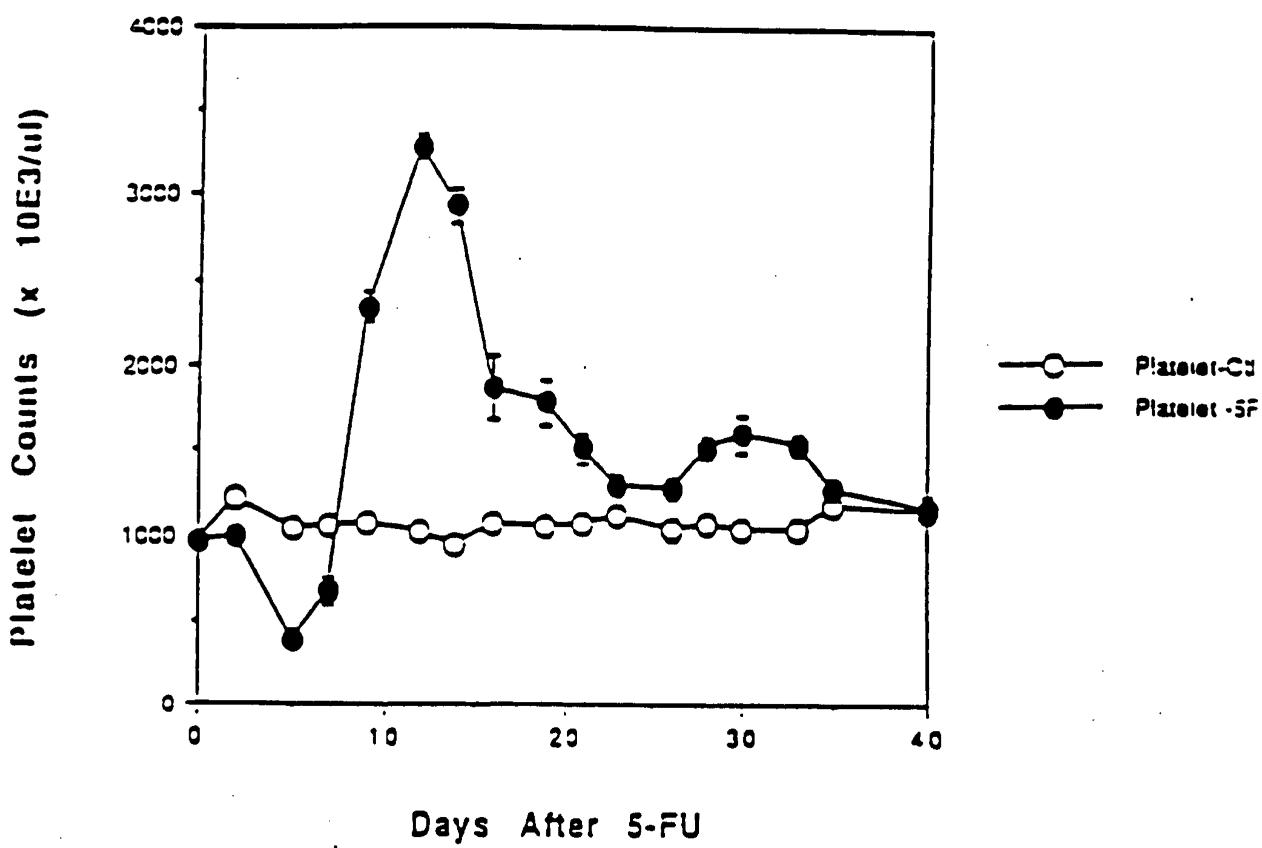
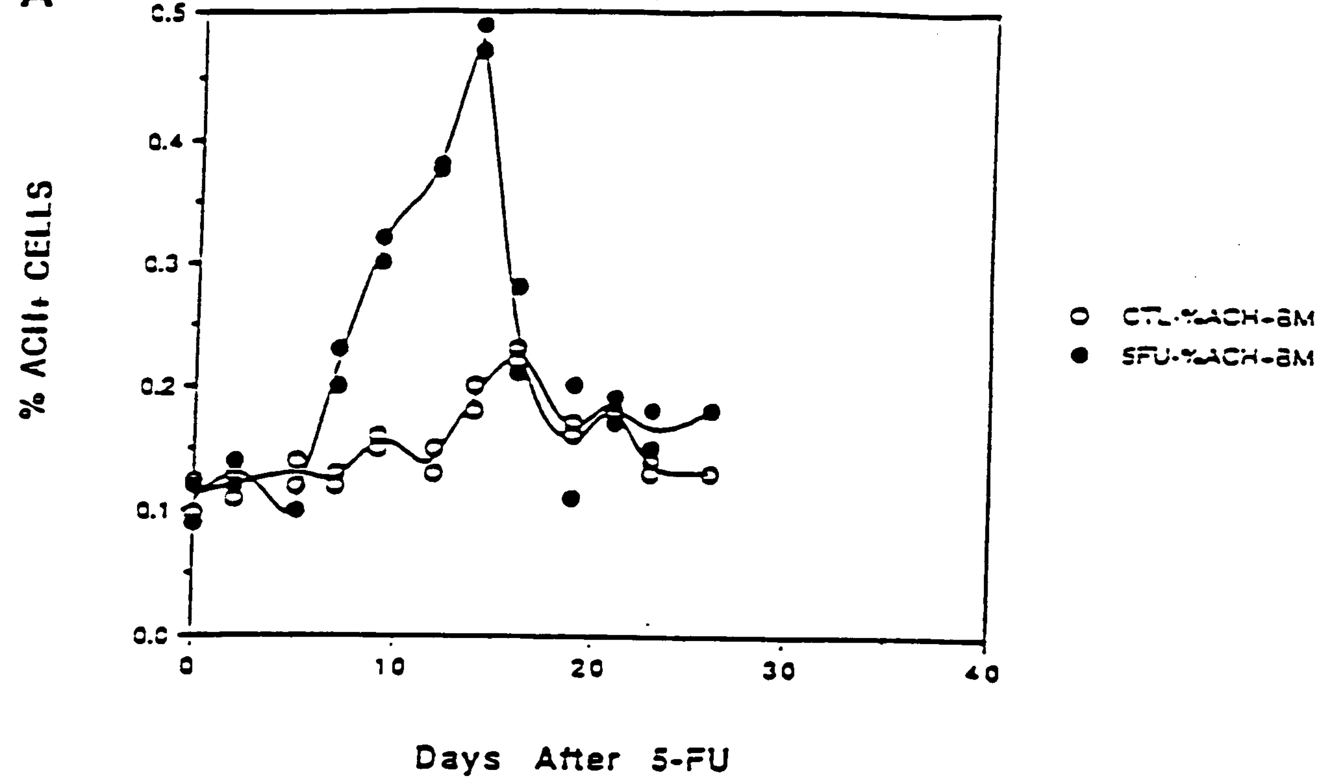


FIG. 56

5-FU Effect on ACH+ Cells in Marrow

A



5-FU Effect on ACH+ Cells in Spleen

B

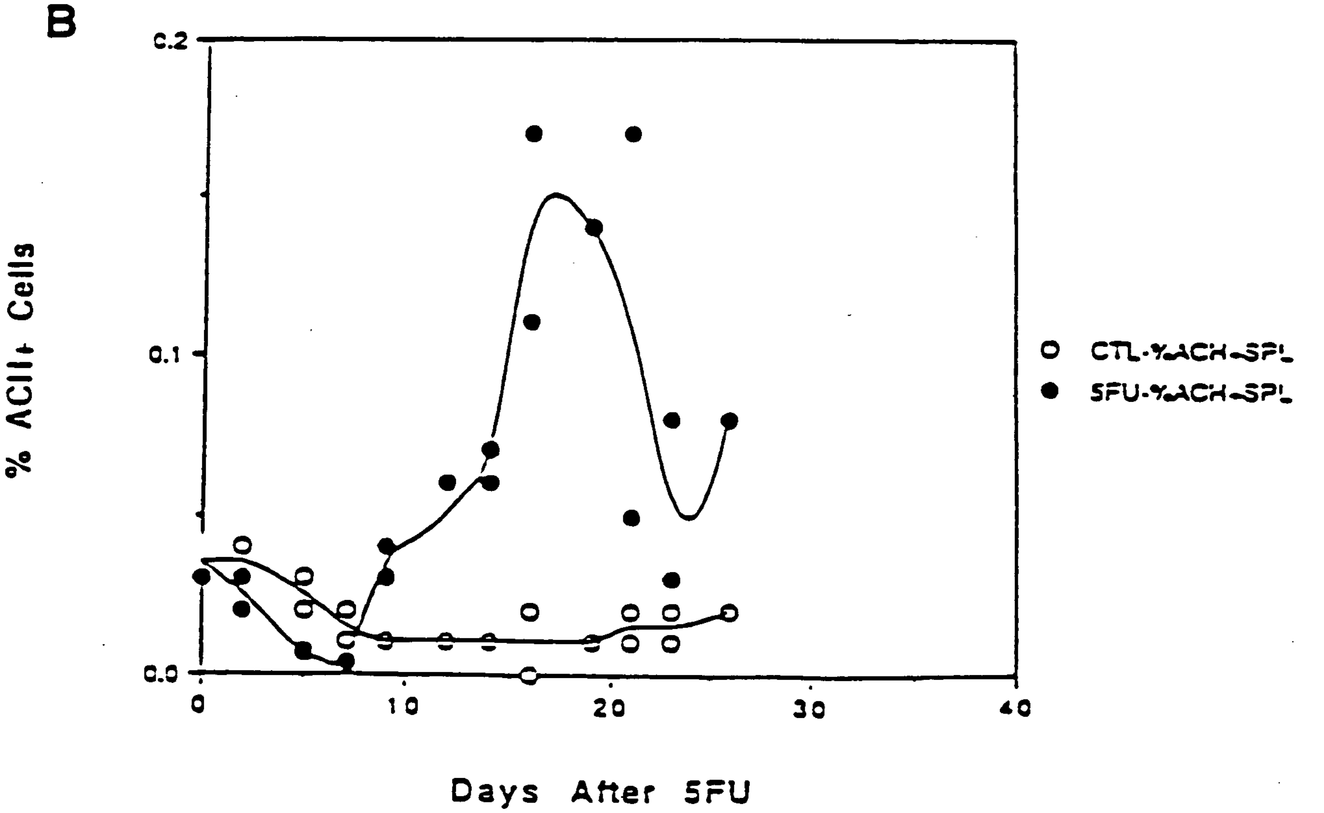
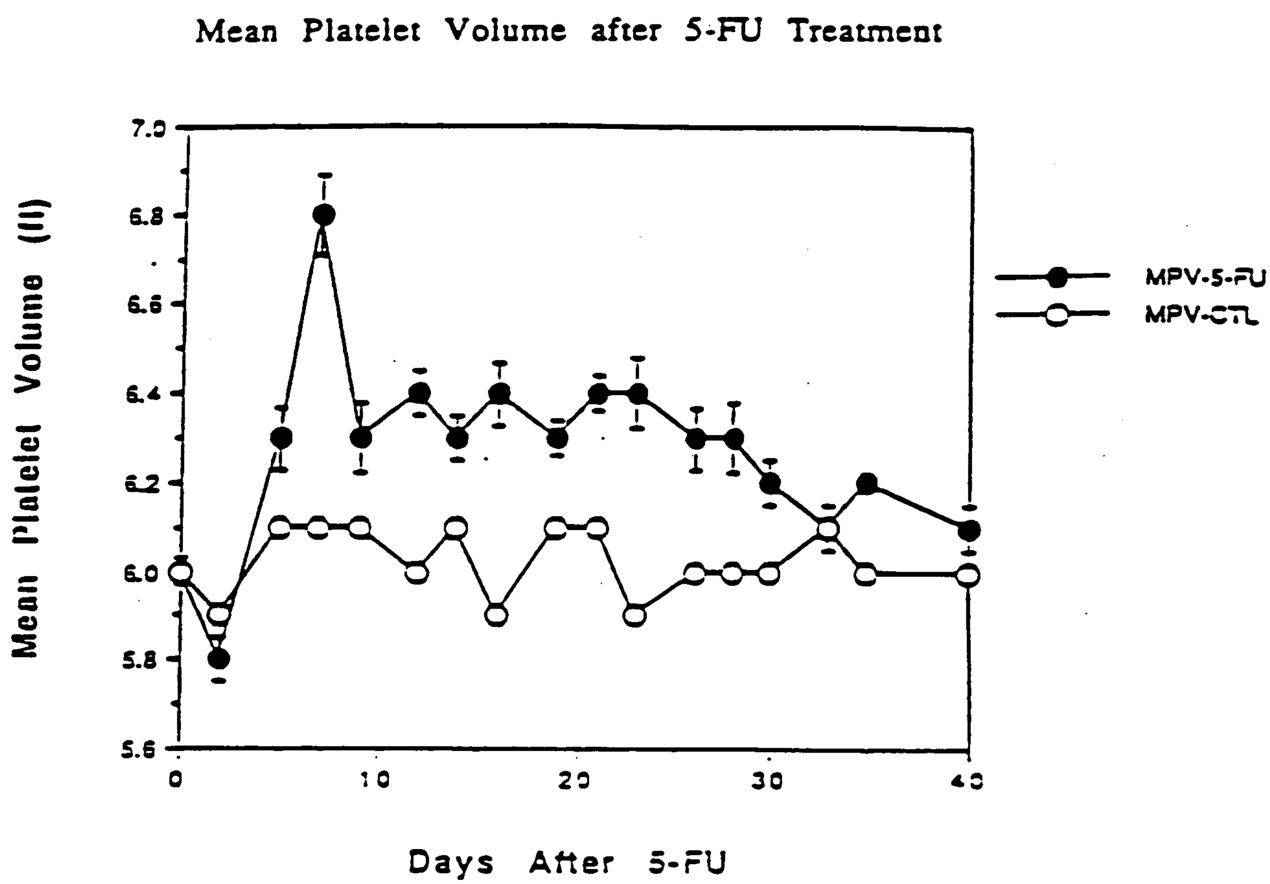
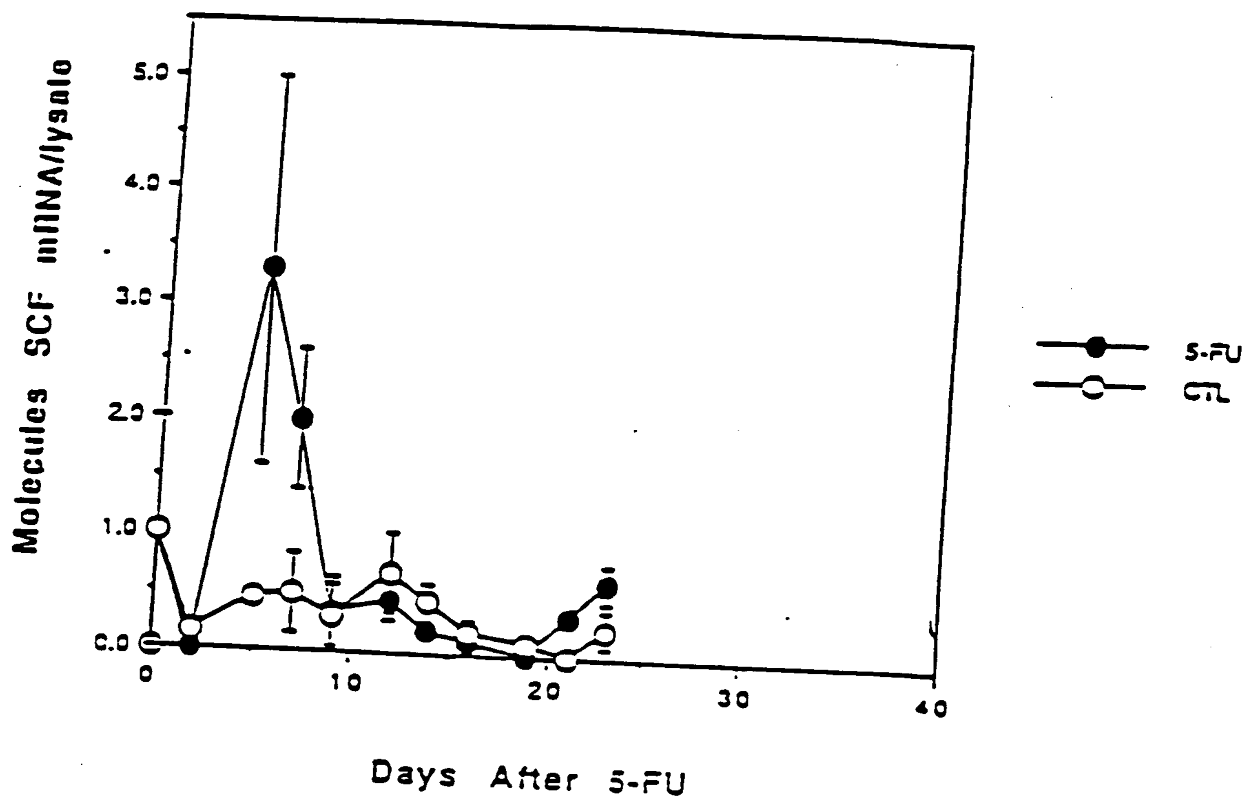


FIG. 57



Mean Platelet Volume after 5-FU Treatment
Mean Platelet Volume (fl)
7.0
6.8
6.6
6.4
6.2
6.0
5.8
5.6
0
10
20
30
40
Days After 5-FU
MPV-5-FU
MPV-CTL

FIG. 58



Molecules SCF mRNA/lysate
5.0
4.0
3.0
2.0
1.0
0.0
0
10
20
30
40
Days After 5-FU
5-FU
CTL

FIG. 59

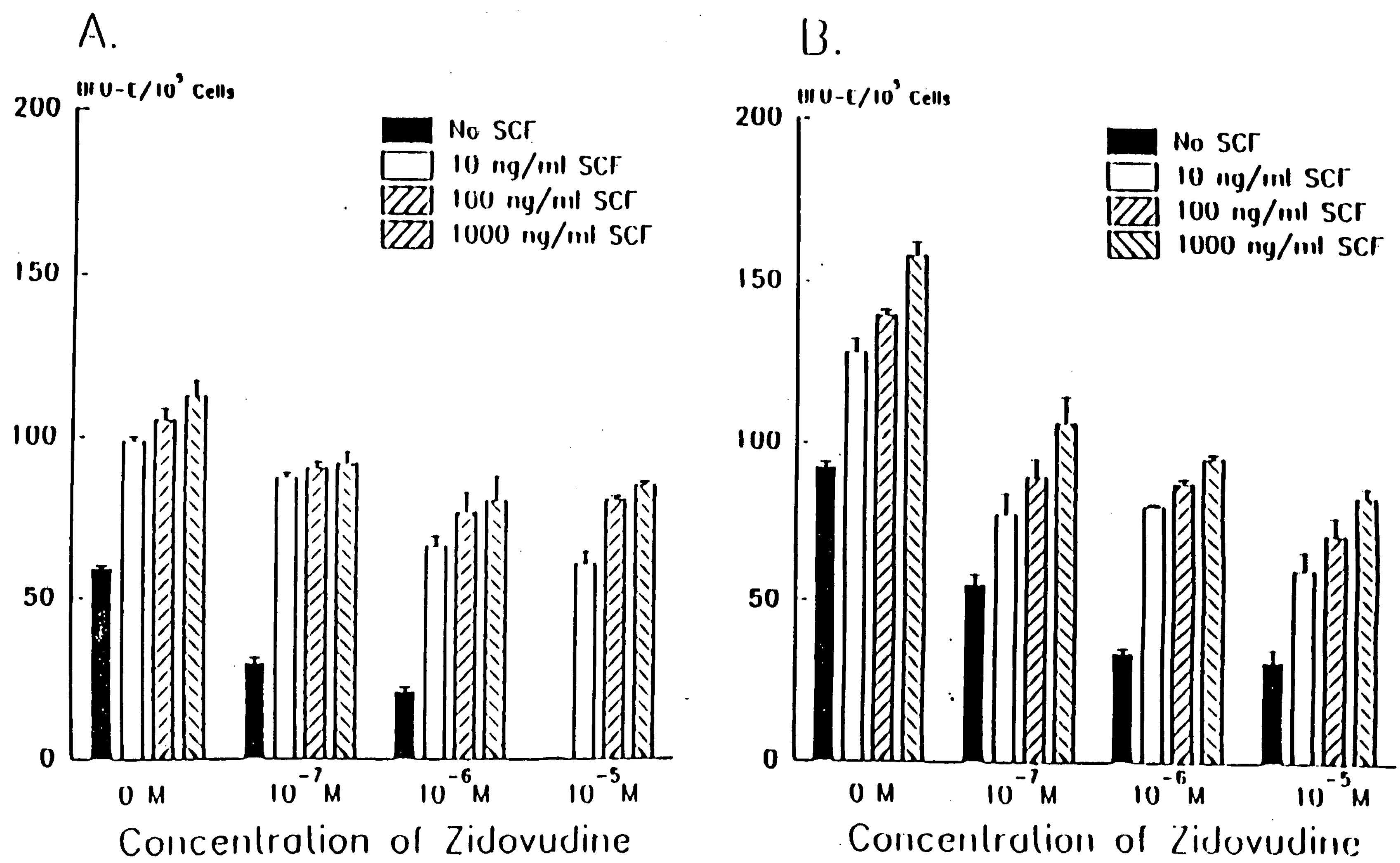

A.
BFU-E/10^5 Cells
200
150
100
50
0
No SCF
10 ng/ml SCF
100 ng/ml SCF
1000 ng/ml SCF
0 M
10^-7 M
10^-6 M
10^-5 M
Concentration of Zidovudine
B.
BFU-E/10^5 Cells
200
150
100
50
0
No SCF
10 ng/ml SCF
100 ng/ml SCF
1000 ng/ml SCF
0 M
10^-7 M
10^-6 M
10^-5 M
Concentration of Zidovudine

FIG. 60

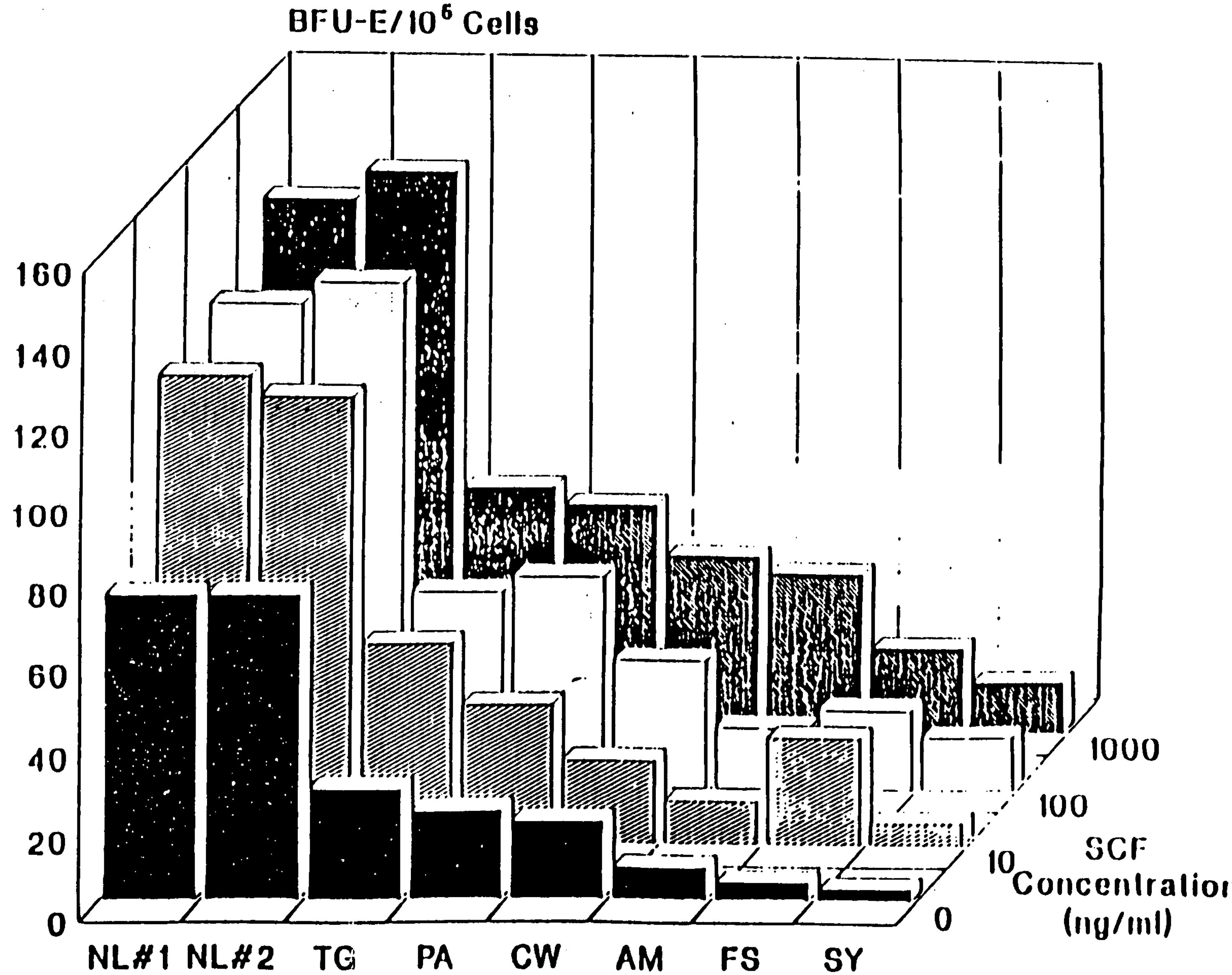
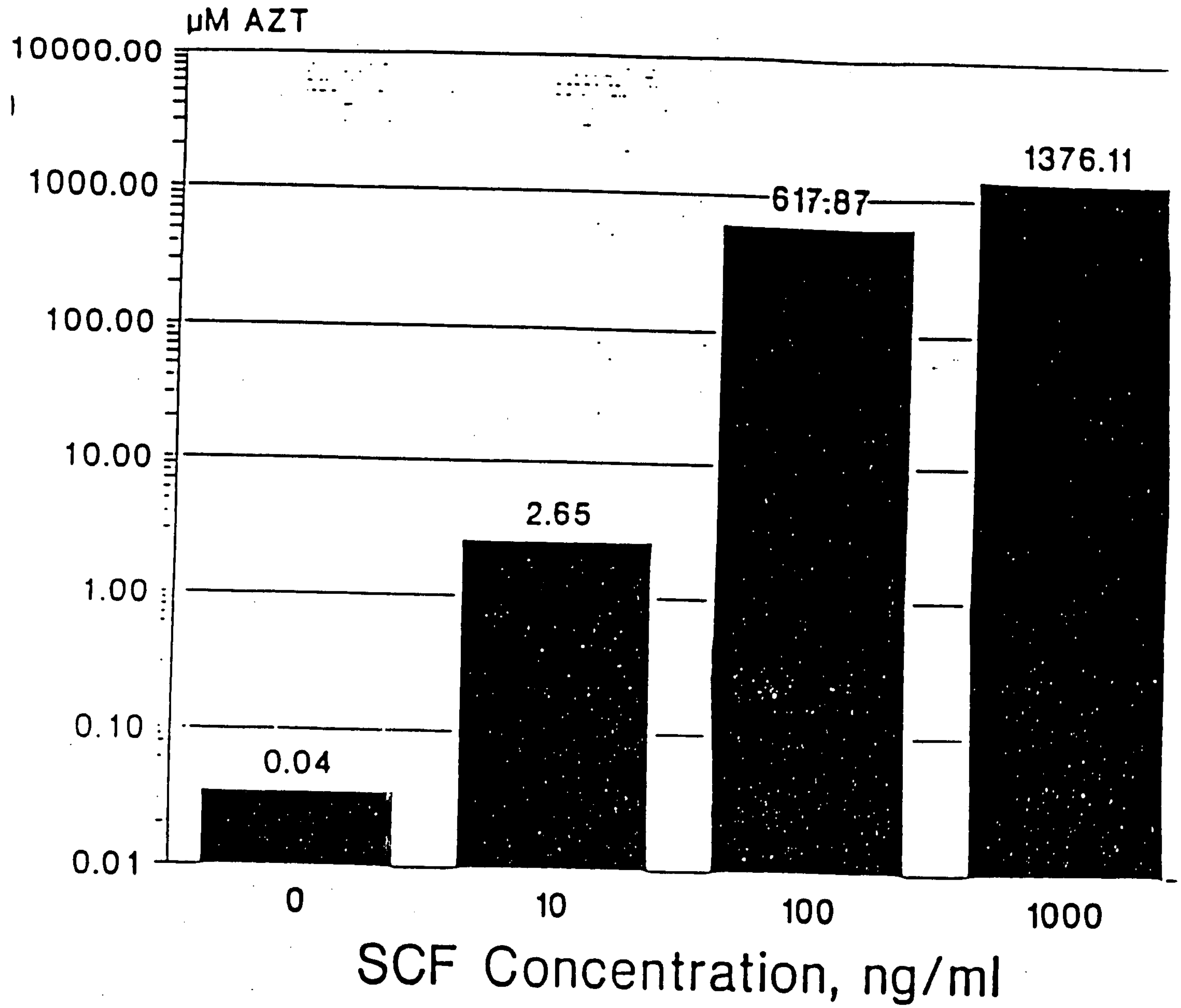

BFU-E/10^6 Cells
160
140
120
100
80
60
40
20
0
NL#1
NL#2
TG
PA
CW
AM
FS
SY
1000
100
10
0
SCF
Concentration
(ng/ml)

FIG. 61



μM AZT
10000.00
1000.00
100.00
10.00
1.00
0.10
0.01
0.04
2.65
617.87
1376.11
0
10
100
1000
SCF Concentration, ng/ml

FIG. 62

EFFECT OF SCF ON AZT SUPPRESSION OF BMC

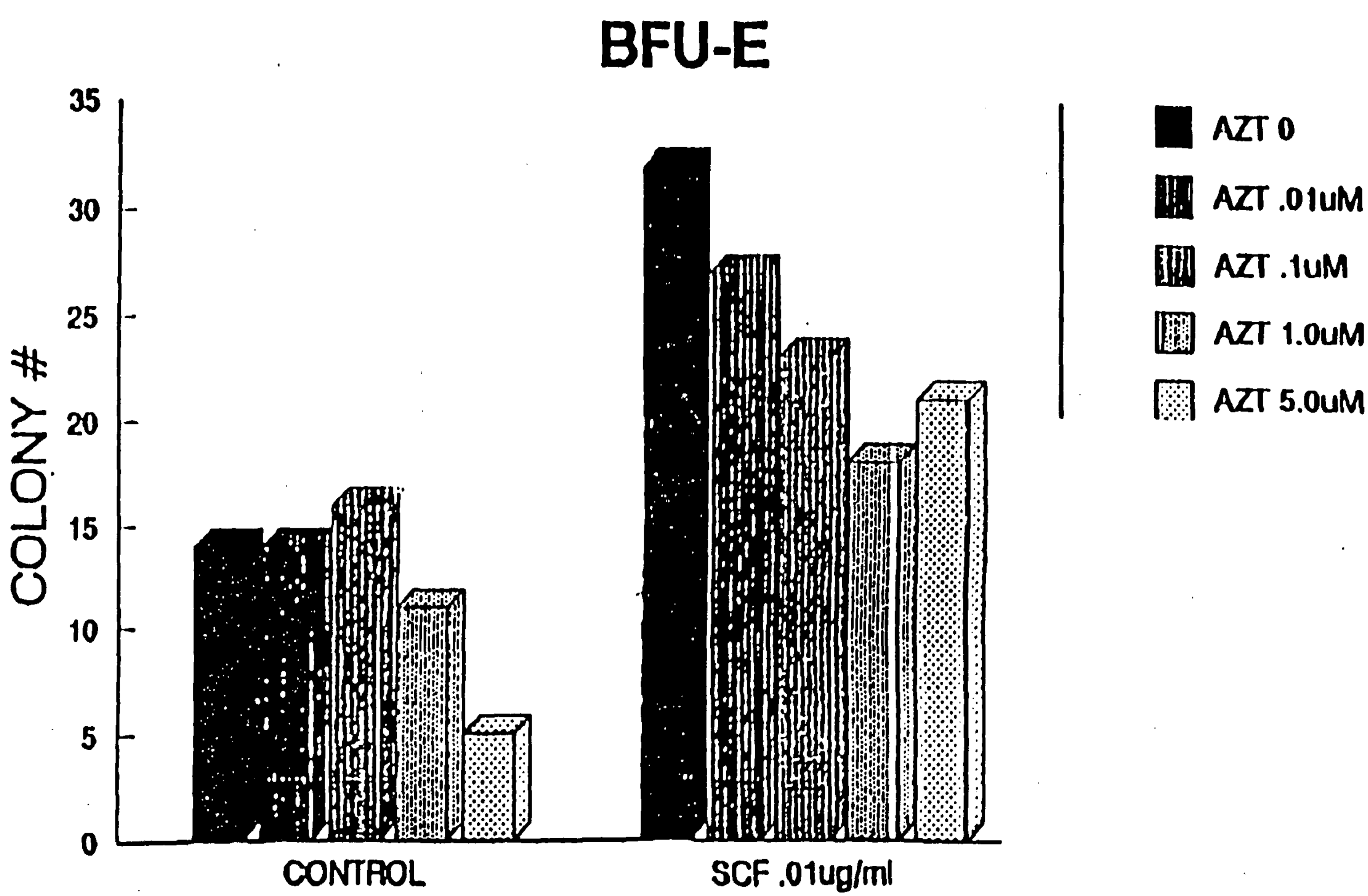


FIG. 63

EFFECT OF SCF ON AZT SUPPRESSION OF BMC

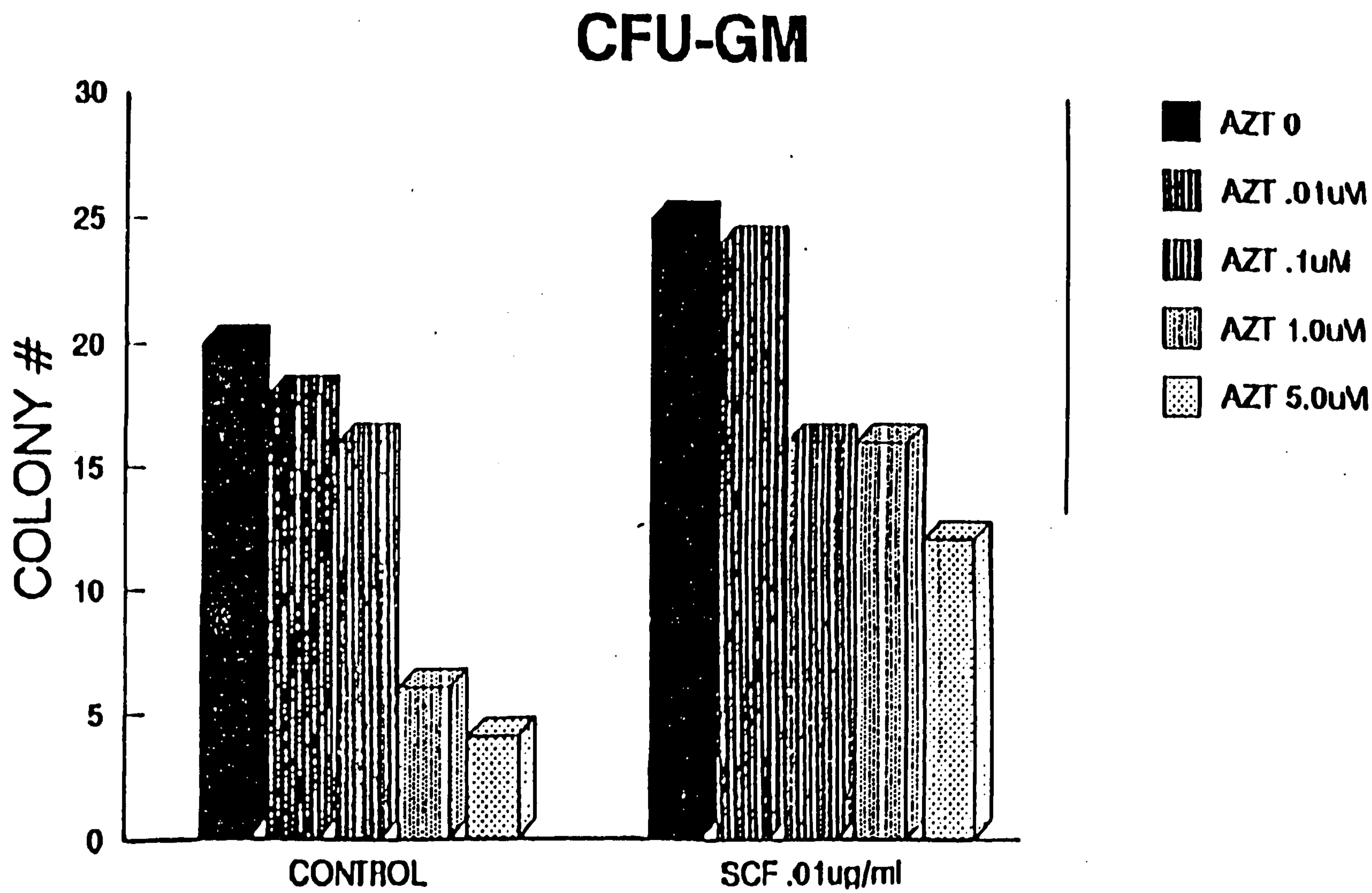


FIG. 64

EFFECT OF SCF ON GANCICLOVIR SUPPRESSION OF BMC

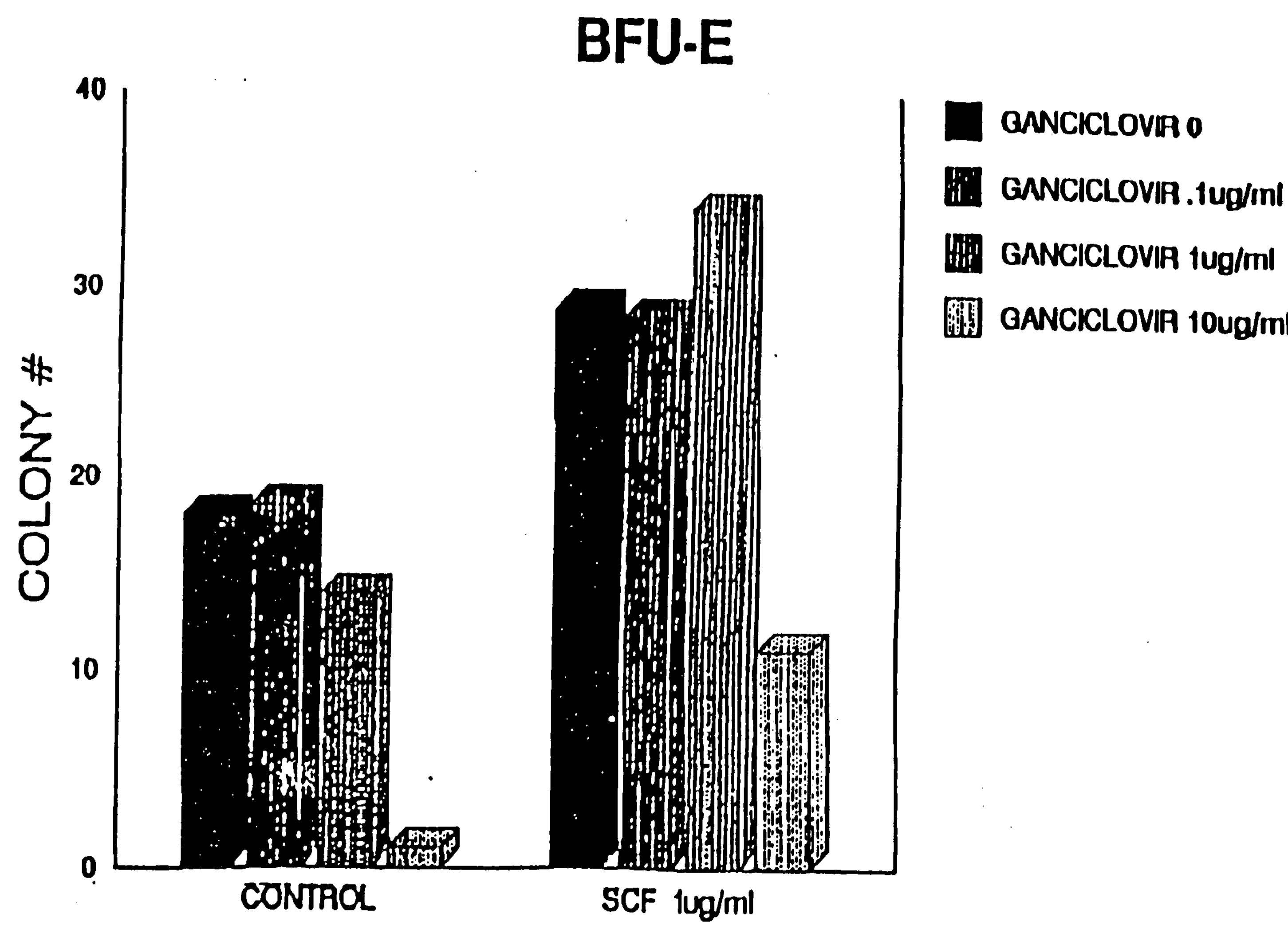


FIG. 65

EFFECT OF SCF ON GANCICLOVIR SUPPRESSION OF BMC

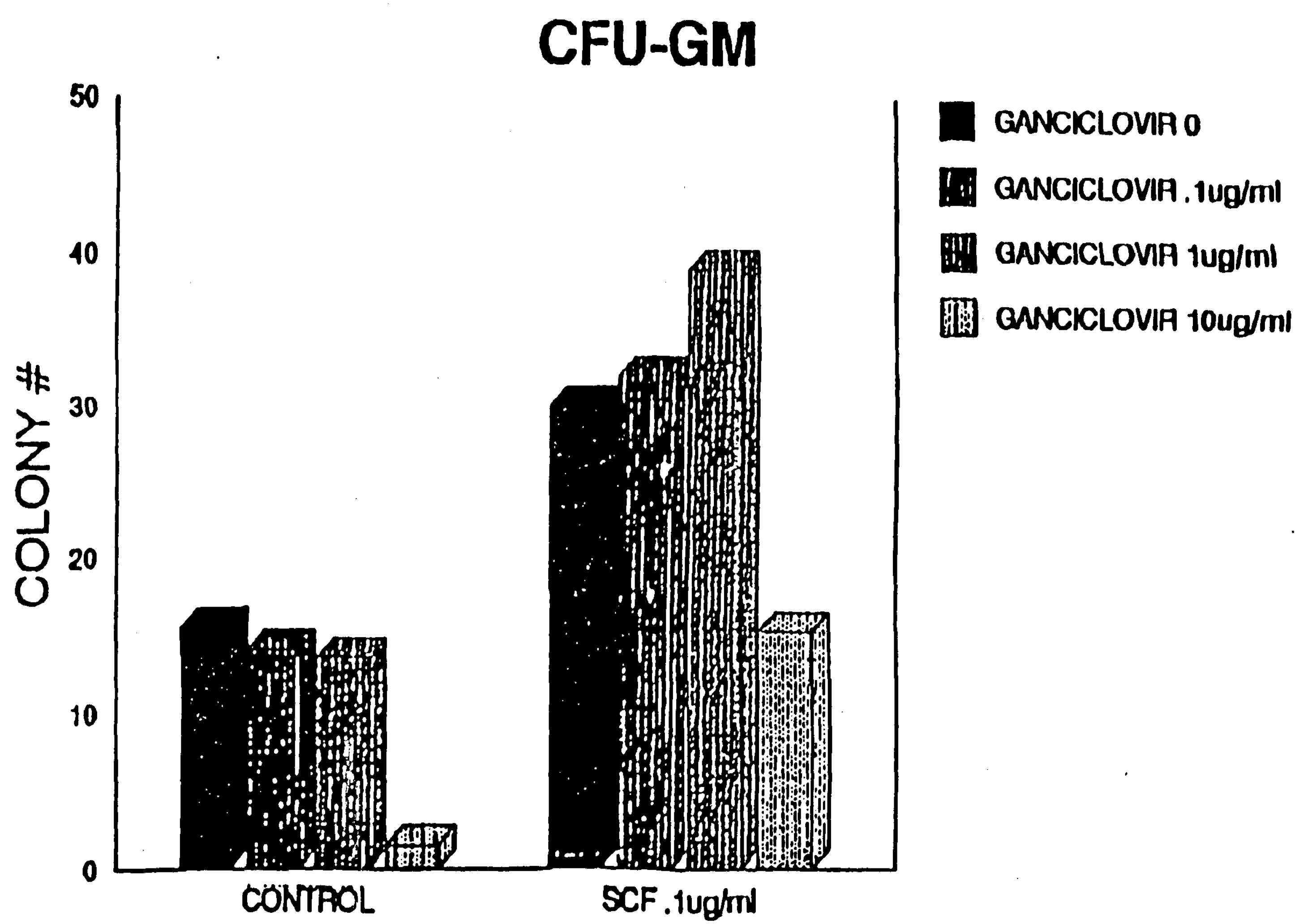


FIG. 66

Effects of SCF on CFU-S Number

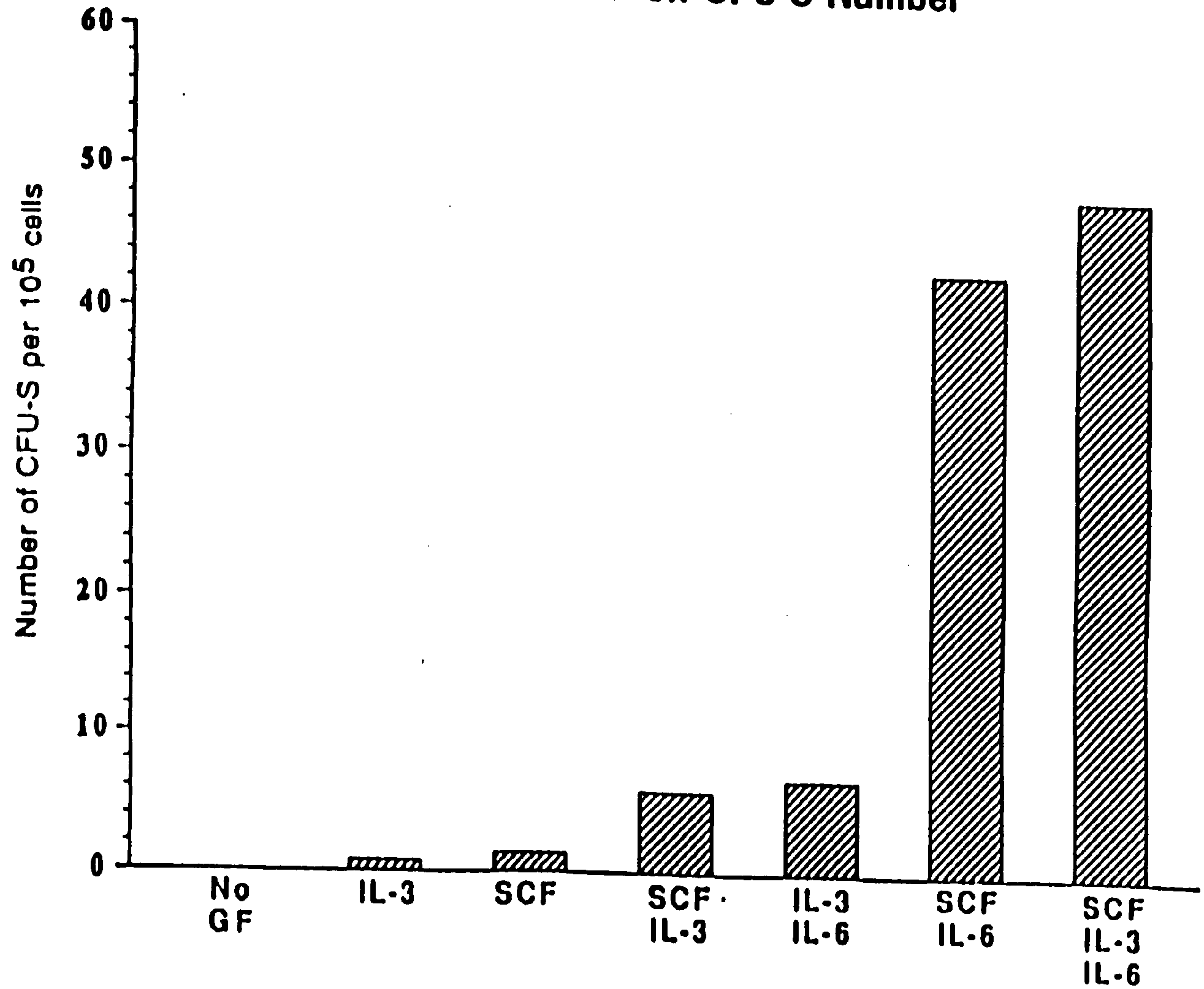
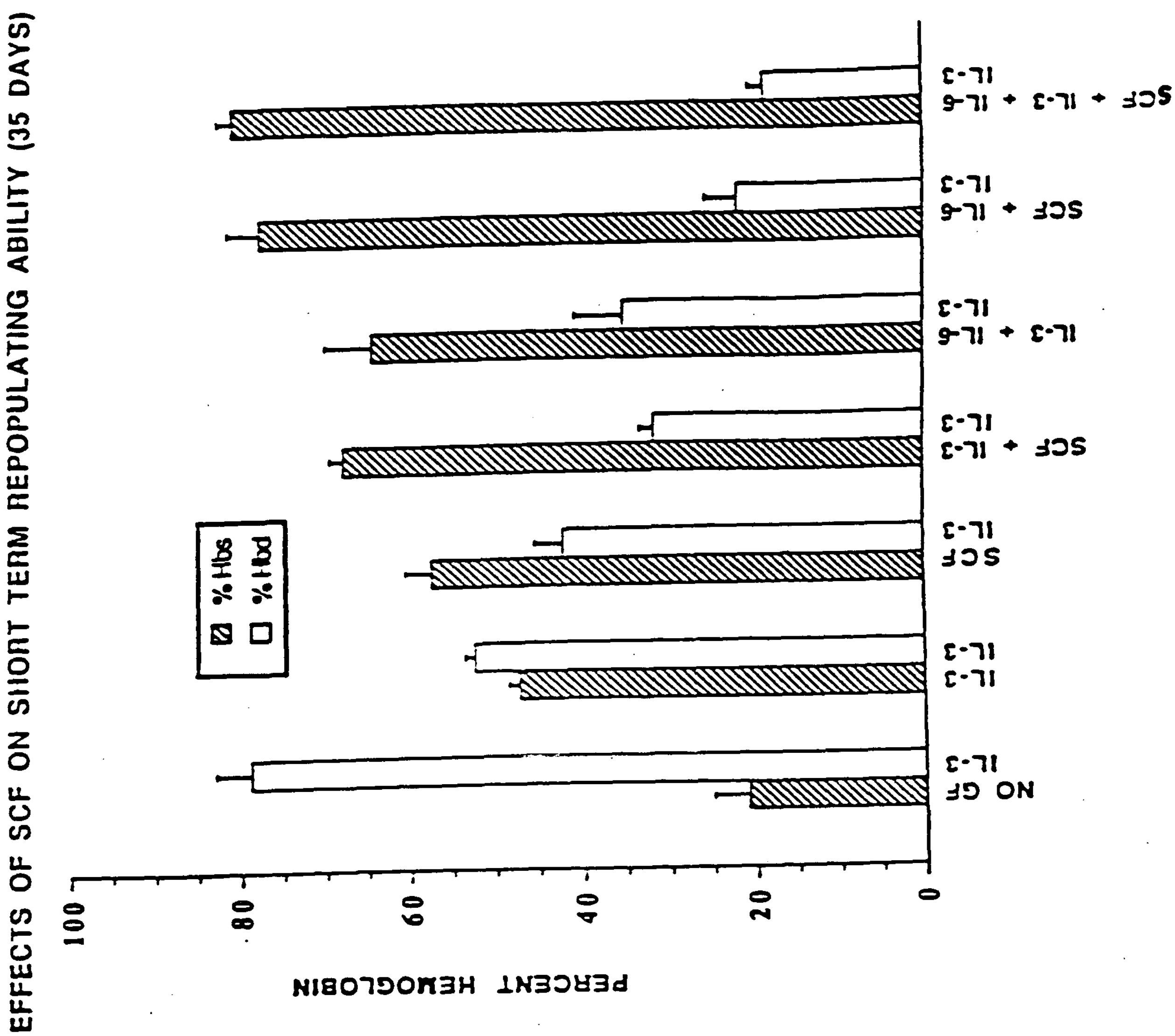
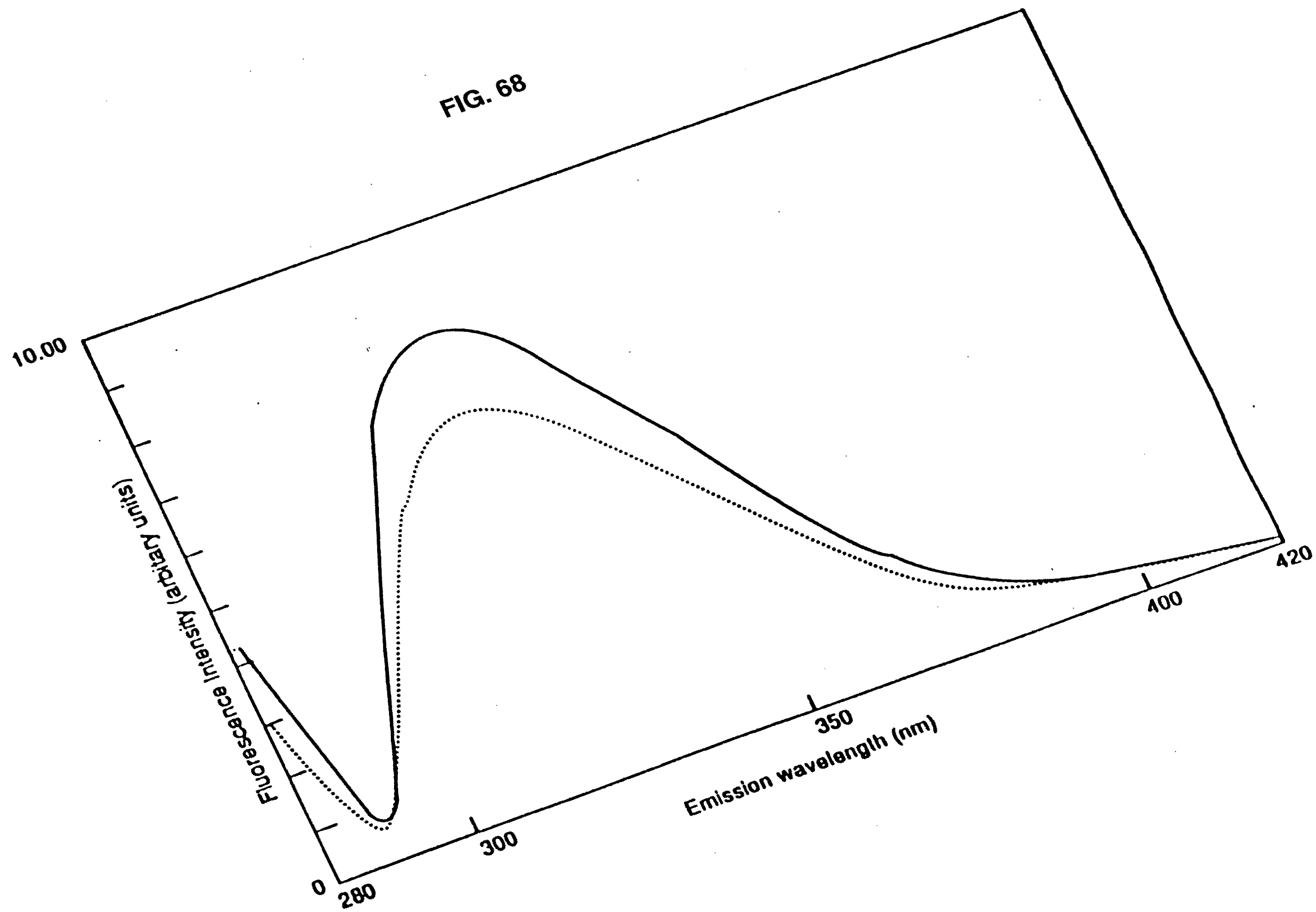


FIG. 67



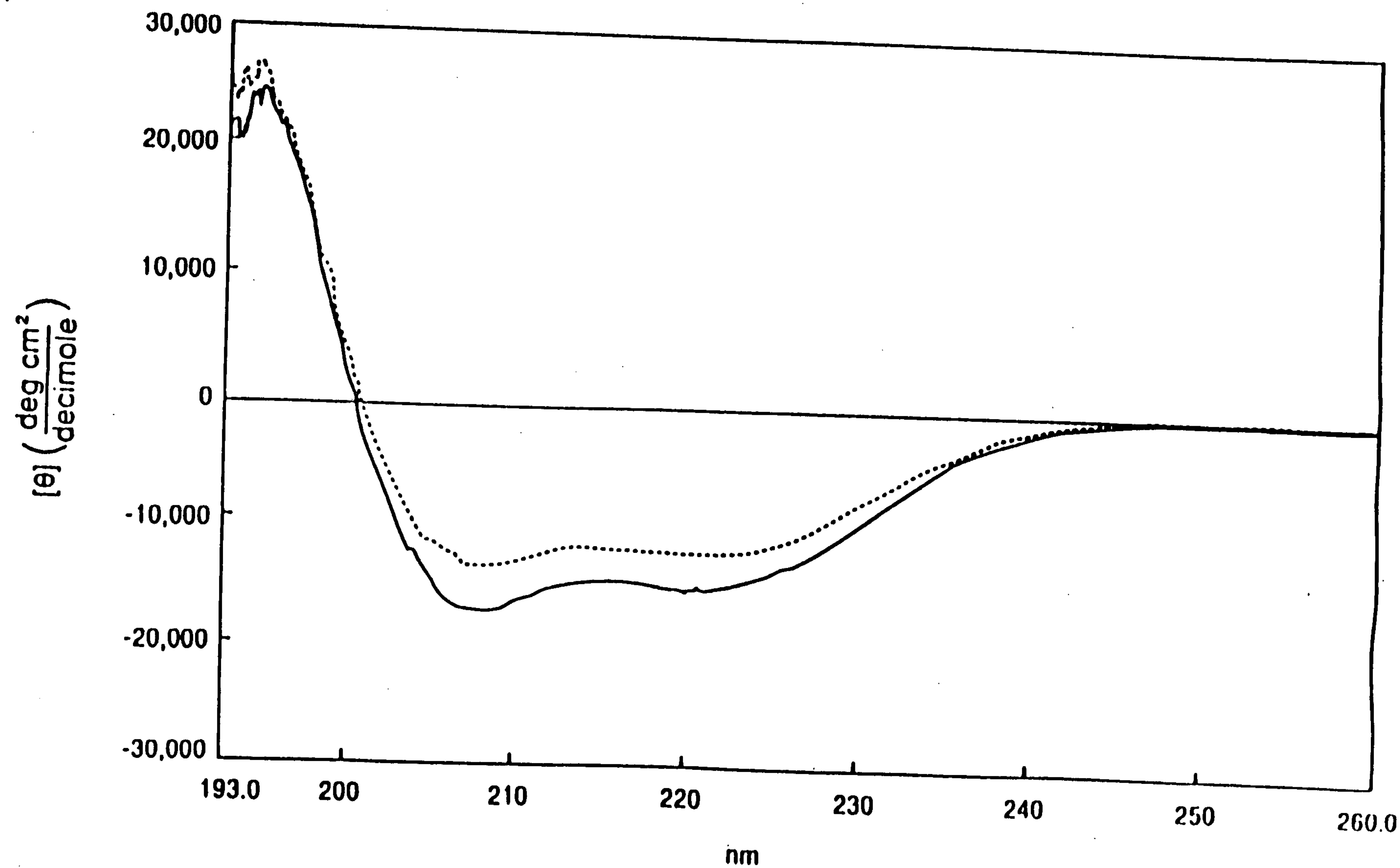
EFFECTS OF SCF ON SHORT TERM REPOPULATING ABILITY (35 DAYS)
PERCENT HEMOGLOBIN
0
20
40
60
80
100
% Hbs
% Hbd
NO GF
IL-3
IL-3
IL-3
SCF
IL-3
SCF + IL-3
IL-3
IL-3 + IL-6
IL-3
SCF + IL-6
IL-3
SCF + IL-3 + IL-6
IL-3

FIG. 68



10.00
0
Fluorescence Intensity (arbitary units)
280
300
350
400
420
Emission wavelength (nm)

FIG. 69A



30,000
20,000
10,000
0
-10,000
-20,000
-30,000
[θ] (deg cm² / decimole)
193.0
200
210
220
230
240
250
260.0
nm

FIG. 69B

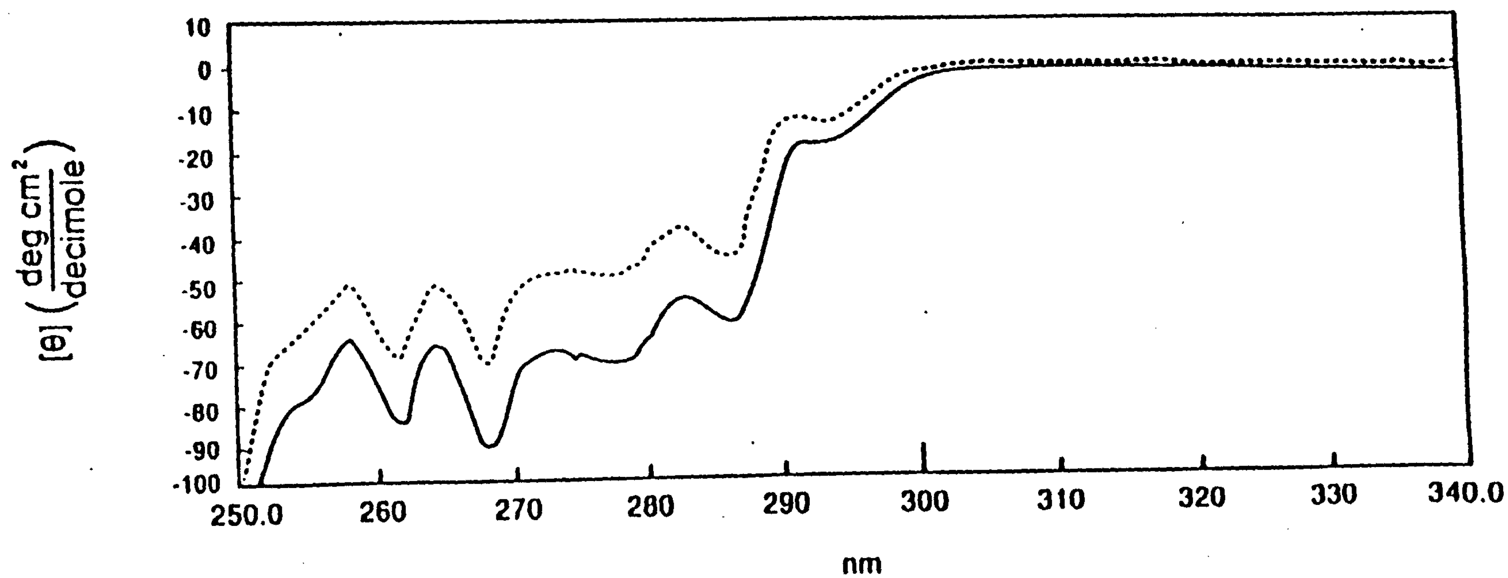

10
0
-10
-20
-30
-40
-50
-60
-70
-80
-90
-100
[θ] (deg cm²/decimole)
250.0
260
270
280
290
300
310
320
330
340.0
nm

FIG. 70